GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:19:09 ; Search time 62 Seconds
(without alignments)
3823.506 Million cell updates/sec

Title: US-09-966-147-6
Perfect score: 4497
Sequence: 1 MDVSLCPAKCSFWRIFLLGS.....IYKILHALGKATPIYLDILG 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4497	100.0	839	2	AAR81625	Aar81625 Human trk
2	4497	100.0	839	3	AAY51601	Aay51601 Human trk
3	4492	99.9	839	5	AAE27937	Aae27937 Human Trk
4	4492	99.9	839	7	ABR82955	Abr82955 Human Trk
5	4488	99.8	839	5	AAM50853	Aam50853 Human rec
6	4436.5	98.7	830	2	AAR81627	Aar81627 Human trk
7	4391	97.6	825	2	AAR81631	Aar81631 Human trk
8	4381	97.4	825	2	AAY06595	Aay06595 Neurotrop
9	4358.5	96.9	864	5	AAM50852	Aam50852 Rat recep
10	4328	96.2	808	5	AAU81284	Aau81284 Human trk
11	4299	95.6	839	2	AAR71621	Aar71621 Porcine T
12	4222	93.9	850	2	AAW11942	Aaw11942 gD.trkC f
13	4193	93.2	825	2	AAR62021	Aar62021 Porcine T
14	4190	93.2	825	2	AAR27148	Aar27148 Adult por
15	4190	93.2	825	2	AAR30883	Aar30883 trkC gene
16	3673	81.7	728	2	AAR27149	Aar27149 Mouse trk
17	3673	81.7	728	2	AAR30884	Aar30884 Partial t
18	3673	81.7	728	2	AAR62022	Aar62022 Murine Tr
19	3563.5	79.2	739	2	AAR71618	Aar71618 Murine Tr
20	2836	63.1	612	3	AAY51602	Aay51602 Human tru
21	2673	59.4	584	2	AAR81626	Aar81626 Human trk
22	2602	57.9	504	2	AAR71619	Aar71619 Porcine T
23	2287.5	50.9	821	5	AAE27935	Aae27935 Mouse ful
24	2287.5	50.9	821	5	AAM50850	Aam50850 Rat recep
25	2287.5	50.9	821	7	ADB79771	Adb79771 Rat neura
26	2287.5	50.9	821	7	ABR82953	Abr82953 Mouse Trk
27	2277	50.6	822	2	AAR81630	Aar81630 Human trk
28	2277	50.6	822	3	AAY51599	Aay51599 Human trk
29	2277	50.6	822	5	AAE27931	Aae27931 Human Trk
30	2277	50.6	822	5	AAM50851	Aam50851 Human rec
31	2277	50.6	822	6	ABU56698	Abu56698 Lung canc
32	2277	50.6	822	7	ABR82949	Abr82949 Human Trk
33	2277	50.6	822	7	ADE40445	Ade40445 Human rec
34	2259	50.2	838	6	ABU56699	Abu56699 Lung canc
35	2256.5	50.2	847	2	AAW11941	Aaw11941 gD.trkB f
36	1961	43.6	796	5	AAM50849	Aam50849 Human rec
37	1961	43.6	796	7	ADE60983	Ade60983 Human Pro
38	1961	43.6	796	7	ADE63269	Ade63269 Human Pro
39	1960	43.6	790	3	AAY51603	Aay51603 Human trk
40	1956	43.5	814	2	AAW11940	Aaw11940 gD.trkA f
41	1950	43.4	790	2	AAY26956	Aay26956 Human Trk
42	1913	42.5	799	5	AAM50848	Aam50848 Rat recep
43	1794	39.9	391	2	AAR71620	Aar71620 Murine Tr
44	1559.5	34.7	408	5	ABG95122	Abg95122 Human tra
45	1554	34.6	318	5	ABG95121	Abg95121 Human tra

ALIGNMENTS

RESULT 1
AAR81625
ID AAR81625 standard; protein; 839 AA.
XX
AC AAR81625;
XX
DT 23-MAY-1996 (first entry)
XX
DE Human trkC receptor protein.
XX
KW trkC receptor; tyrosine-kinase; enzyme; protease; inflammation; pain;
KW diagnosis; neurotrophic factor; kidney; lung; psychiatric disorder; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Misc-difference	72. .75
FT		/note= "potential N-linked glycosylation site"
FT	Misc-difference	79. .82
FT		/note= "potential N-linked glycosylation site"
FT	Misc-difference	133. .136
FT		/note= "potential N-linked glycoylation site"
FT	Misc-difference	163. .166
FT		/note= "potential N-linked glycosylation site"
FT	Misc-difference	203. .206
FT		/note= "potential N-linked glycoylation site"
FT	Misc-difference	218. .221
FT		/note= "potential N-linked glycosylation site"
FT	Misc-difference	232. .235
FT		/note= "potential N-linked glycosylation site"
FT	Misc-difference	259. .262
FT		/note= "potential N-linked glycosylation site"
FT	Misc-difference	267. .270
FT		/note= "potential N-linked glycosylation site"
FT	Misc-difference	272. .275
FT		/note= "potential N-linked glycosylation site"
FT	Misc-difference	294. .297
FT		/note= "potential N-linked glycosylation site"
FT	Misc-difference	375. .378
FT		/note= "potential N-linked glycosylation site"
FT	Misc-difference	388. .391
FT		/note= "potential N-linked glycosylation site"
FT	Domain	430. .453
FT		/note= "transmembrane domain"
FT	Misc-difference	529
FT		/note= "splice site resulting in truncated form"
FT	Domain	544. .824
FT		/note= "tyrosine-kinase domain"

XX
PN WO9525795-A1.
XX
PD 28-SEP-1995.
XX
PF 17-MAR-1995; 95WO-US003426.
XX
PR 18-MAR-1994; 94US-00215139.
PR 05-AUG-1994; 94US-00286846.
PR 20-DEC-1994; 94US-00359705.
XX
PA (GETH) GENENTECH INC.
XX
PI Presta LG, Shelton DL, Urfer R;
XX
DR WPI; 1995-344616/44.
DR N-PSDB; AAT00690.
XX
PT New human trkB and trkC poly:peptide(s) and fusion proteins contg. them -
PT also DNA, vectors and transformed cells useful in treatment and diagnosis
PT of abnormal neurotrophic factor expression, e.g. inflammatory pain.
XX
PS Claim 12; Fig 2A; 117pp; English.
XX
CC This DNA sequence may be expressed recombinantly for the production of
CC human trkC receptor, and to detect or amplify trkC genes. The encoded
CC protein may be used as a reagent in kinase receptor activation assays,
CC and therapeutically in diseases associated with over or under expression
CC of neurotrophic factor (e.g. pain of inflammation, kidney, lung,
CC cardiovascular or psychiatric disorders and some sorts of tumours)
XX
SQ Sequence 839 AA;

Query Match 100.0%; Score 4497; DB 2; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
```

RESULT 2
AAY51601
ID AAY51601 standard; protein; 839 AA.
XX
AC AAY51601;
XX
DT 30-MAY-2000 (first entry)
XX
DE Human trkC receptor protein.
XX
KW trkB; human; receptor tyrosine kinase; trkC; diagnosis; neurotrophin;
KW neurotrophic factor.
XX
OS Homo sapiens.
XX
PN US6027927-A.
XX
PD 22-FEB-2000.
XX
PF 01-OCT-1997; 97US-00942562.
XX
PR 18-MAR-1994; 94US-00215139.
PR 05-AUG-1994; 94US-00286846.
PR 19-MAY-1995; 95US-00444597.
XX
PA (GETH) GENENTECH INC.
XX
PI Urfer R, Shelton DL, Presta LG;
XX
DR WPI; 2000-194832/17.
DR N-PSDB; AAZ88841.
XX
PT New human trk receptors useful in the diagnosis of various human
PT pathological conditions associated with elevated or reduced levels of
PT neurotrophins capable of binding trkB and/or trkC.
XX
PS Claim 1; Col 75-80; 78pp; English.
XX
CC This invention describes a novel isolated and purified polypeptide (I),
CC belonging to the trk family of receptor tyrosine kinases, trkB and trkC.
CC (I) are useful in the purification of human neurotrophic factors and in
CC the diagnosis of various human pathological conditions associated with
CC elevated or reduced levels of neurotrophins capable of binding trkB
CC and/or trkC. This sequence represents the human trkC receptor described
CC in the method of the invention
XX
SQ Sequence 839 AA;

Query Match 100.0%; Score 4497; DB 3; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
```

RESULT 3
AAE27937
ID AAE27937 standard; protein; 839 AA.
XX
AC AAE27937;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human TrkC protein.
XX
KW Human; neurodegenerative disorder; neurodevelopmental disorder; TrkB;
KW TrkC; Alzheimer's disease; AD; amyotrophic lateral sclerosis; ALS; PD;
KW Parkinson's disease; Huntington's disease; HD; Lou Gehrig's disease;
KW diabetic peripheral neuropathy; Down's syndrome; DS; neuroprotective;
KW gene therapy; anticonvulsant; cerebroprotective; nootropic.
XX
OS Homo sapiens.
XX
PN WO200267858-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-US005151.
XX
PR 22-FEB-2001; 2001US-0270553P.
XX
PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI Krueger BK, Kingsbury TJ, Bambrick LL, Dorsey SG;
XX
DR WPI; 2002-698627/75.
DR N-PSDB; AAD45792.
XX
PT Treating and/or preventing neurodegenerative and neurodevelopmental
PT disorders such as Alzheimer's, Parkinson's and Huntington's diseases by
PT altering the ratio of amount of full-length and truncated TrkB or TrkC
PT polypeptides.
XX
PS Disclosure; Page 88-92; 96pp; English.
XX
CC The present invention relates to a method of treating neurodegenerative
CC or neurodevelopmental disorders in a mammal which involves administering
CC an isolated nucleic acid encoding a full-length TrkB or TrkC or their
CC mutant, variant, homologue or fragment or an anti-sense RNA for truncated
CC TrkB or TrkC isoforms, where they increase the amount of full-length TrkB
CC or TrkC or decrease the amount of truncated TrkB or TrkC in treated
CC neurons. The methods and compositions of the invention are useful for
CC treating or preventing neurodegenerative or neurodevelopmental disorders
CC such as Alzheimer's disease (AD), Parkinson's disease (PD), Huntington's
CC disease (HD), amyotrophic lateral sclerosis (ALS; Lou Gehrig's disease),
CC diabetic peripheral neuropathy, the adverse complications of Down's
CC syndrome (DS) and other types of peripheral neuropathy. Sequences of the
CC invention are also used in gene therapy. The present sequence is human
CC TrkC protein
XX
SQ Sequence 839 AA;

Query Match 99.9%; Score 4492; DB 5; Length 839;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 838; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
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Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
```

RESULT 4
ABR82955
ID ABR82955 standard; protein; 839 AA.
XX
AC ABR82955;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human TrkC polypeptide.
XX
KW TrkB; TrkC; neurodegenerative; neuro-developmental; antiparkinsonian;
KW neuroprotective; anticonvulsant; cerebroprotective; vasotropic;
KW nootropic; human.
XX
OS Homo sapiens.
XX
PN WO2003071872-A1.
XX
PD 04-SEP-2003.
XX
PF 28-MAY-2002; 2002WO-US016807.
XX
PR 22-FEB-2002; 2002WO-US005151.
XX
PA (UYMA-) UNIV MARYLAND BALTIMORE.
PA (KRUE/) KRUEGER B K.
PA (KING/) KINGSBURY T J.
PA (BAMB/) BAMBRICK L L.
PA (DORS/) DORSEY S G.
XX
PI Krueger BK, Kingsbury TJ, Bambrick LL, Dorsey SG;
XX
DR WPI; 2003-731549/69.
DR N-PSDB; ACF36571.
XX
PT Treating and/or preventing neurodegenerative or neuro-developmental
PT disorders, such as Alzheimer's disease, Parkinson's disease and
PT amyotrophic lateral sclerosis, using nucleic acids encoding TrkB and/or
PT TrkC polypeptides.
XX
PS Disclosure; Page 89-92; 99pp; English.
XX
CC The invention relates to treating a neurodegenerative or neuro-
CC developmental disorder in a mammal. The method involves altering the
CC ratio of the amount of full length TrkB polypeptide to the amount of
CC truncated TrkB polypeptides in a neuron or by altering the ratio of the
CC amount of full length TrkC polypeptide to the amount of truncated TrkC
CC polypeptides in a neuron. The methods and compositions of the present
CC invention are useful for treating and/or preventing a neurodegenerative
CC or neuro-developmental disorder, such as Alzheimer's disease, Parkinson's
CC disease, Huntington's disease, amyotrophic lateral sclerosis (Lou
CC Gehrig's disease), the adverse neurologic complications of Down syndrome,
CC diabetic peripheral neuropathy and other types of peripheral neuropathy,
CC and is associated with an injury to the central or peripheral nervous
CC system resulting from stroke, cerebral ischaemia, or chemical and/or
CC physical trauma. The present sequence represents a human TrkC polypeptide
CC (GenBank Accession No. XM_038336)
XX
SQ Sequence 839 AA;

```
  Query Match             99.9%;  Score 4492;  DB 7;  Length 839;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  838;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANININITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASININITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
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Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839

RESULT 5
AAM50853
ID   AAM50853 standard; protein; 839 AA.
XX
AC   AAM50853;
XX
DT   01-MAY-2002  (first entry)
XX
DE   Human receptor tyrosine kinase TrkC.
XX
KW   Receptor tyrosine kinase; TrkC; receptor; human; neurotrophin-3;
KW   Huntington's disease; Parkinson's disease; Alzheimer's disease;
KW   amyotrophic lateral sclerosis; neurodegenerative disease; cancer;
KW   neuroprotective; nootropic; anticonvulsant; antiparkinsonian; enzyme;
KW   cytostatic; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .31
FT                   /label= Signal_peptide
FT   Protein         32. .839
FT                   /label= Mature_protein
FT   Domain          32. .429
FT                   /label= Extracellular
FT   Misc-difference 70
FT                   /note= "may be replaced by Ser"
FT   Modified-site   72
FT                   /note= "N-glycosylated"
FT   Modified-site   79
FT                   /note= "N-glycosylated"
FT   Modified-site   133
FT                   /note= "N-glycosylated"
FT   Modified-site   163
FT                   /note= "N-glycosylated"
FT   Modified-site   203
FT                   /note= "N-glycosylated"
FT   Modified-site   218
FT                   /note= "N-glycosylated"
FT   Domain          227. .288
FT                   /label= Ig-like_C2-type
FT   Modified-site   232
FT                   /note= "N-glycosylated"
FT   Modified-site   259
FT                   /note= "N-glycosylated"
FT   Modified-site   267
FT                   /note= "N-glycosylated"
FT   Modified-site   272
FT                   /note= "N-glycosylated"
FT   Modified-site   294
FT                   /note= "N-glycosylated"
FT   Domain          319. .382
FT                   /label= Ig-like_C2-type
FT   Modified-site   375
FT                   /note= "N-glycosylated"
FT   Modified-site   388
FT                   /note= "N-glycosylated"
FT   Misc-difference 402. .410
FT                   /note= "missing in isoform D"
FT   Domain          430. .453
FT                   /label= Transmembrane
FT   Domain          454. .839
FT                   /label= Cytoplasmic
FT   Binding-site    516
FT                   /note= "interaction with SHC protein"
FT   Modified-site   516
FT                   /note= "O-phosphorylated"
FT   Misc-difference 529. .612
FT                   /note= "replaced by WVFSNIDNHGILNLKDNRDHLVPSTHYIYEE
FT                   PEVQSGEVSYPRSHGFREIMLNPISLPGHSKPLNHGIYVEDVN VYFSKGRHGF in
FT                   isoform B"
FT   Domain          538. .839
FT                   /label= Protein_kinase
FT   Region          544. .552
FT                   /note= "ATP binding site"
FT   Region          572
FT                   /note= "ATP binding site"
FT   Misc-difference 613. .839
FT                   /note= "missing in isoform B"
FT   Misc-difference 635
FT                   /note= "may be replaced by Asn"
FT   Active-site     679
FT   Modified-site   705
FT                   /note= "O-phosphorylated"
FT   Modified-site   709
FT                   /note= "O-phosphorylated"
FT   Modified-site   710
FT                   /note= "O-phosphorylated"
FT   Misc-difference 712. .725
FT                   /note= "missing in isoform C"
FT   Binding-site    834
FT                   /note= "interaction with PLC-gamma-1"
FT   Modified-site   834
FT                   /note= "O-phosphorylated"
XX
PN   WO200203071-A2.
XX
PD   10-JAN-2002.
XX
PF   05-JUL-2001; 2001WO-US021472.
XX
PR   05-JUL-2000; 2000US-0215778P.
XX
PA   (PANG-) PANGENE CORP.
XX
PI   Bates AT;
XX
DR   WPI; 2002-179638/23.
XX
PT   Screening for a neurotrophic factor mimetic, useful for treating, e.g.,
PT   cancer and Alzheimer's, comprises combining a candidate mimetic with a
PT   fragment of a tyrosine kinase protein.
XX
PS   Disclosure; Fig 13A; 107pp; English.
XX
CC   The present sequence is that of human receptor tyrosine kinase TrkC, the
CC   receptor for neurotrophin-3 (NT-3). The invention concerns Trks and their
CC   ligands that modulate cell growth, differentiation and survival. Trk
CC   proteins are known to mediate the activities of neurotrophins and are
CC   also known proto-oncogenes. Methods are claimed for screening for small
CC   molecule neurotrophic factor (NTF) mimetics, such as the cyclic peptide
CC   given in AAM50844, capable of binding to a Trk protein or of modulating
CC   the binding of a neurotrophin to a Trk protein. Also claimed are
CC   medicaments comprising a small molecule NTF mimetic and their use in
CC   claimed methods for treatment of cancer or a neurodegenerative disease
CC   selected from Huntington's disease, Parkinson's disease, Alzheimer's
CC   disease and amyotrophic lateral sclerosis
XX
SQ   Sequence 839 AA;

  Query Match             99.8%;  Score 4488;  DB 5;  Length 839;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  838;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
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Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDG 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
```

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RESULT 6
AAR81627
ID   AAR81627 standard; protein; 830 AA.
XX
AC   AAR81627;
XX
DT   08-JUL-1996  (first entry)
XX
DE   Human trkC receptor protein mutant.
XX
KW   trkC receptor; tyrosine-kinase; enzyme; protease; inflammation; pain;
KW   diagnosis; neurotrophic factor; kidney; lung; psychiatric disorder.
XX
OS   Homo sapiens.
XX
PN   WO9525795-A1.
XX
PD   28-SEP-1995.
XX
PF   17-MAR-1995;    95WO-US003426.
XX
PR   18-MAR-1994;    94US-00215139.
PR   05-AUG-1994;    94US-00286846.
PR   20-DEC-1994;    94US-00359705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Presta LG,  Shelton DL,  Urfer R;
XX
DR   WPI; 1995-344616/44.
XX
PT   New human trkB and trkC poly:peptide(s) and fusion proteins contg. them -
PT   also DNA, vectors and transformed cells useful in treatment and diagnosis
PT   of abnormal neurotrophic factor expression, e.g. inflammatory pain.
XX
PS   Claim 14; Fig 2A; 117pp; English.
XX
CC   This DNA sequence may be expressed recombinantly for the production of
CC   human trkC receptor, and to detect or amplify trkC genes. The encoded
CC   protein may be used as a reagent in kinase receptor activation assays,
CC   and therapeutically in diseases associated with over or under expression
CC   of neurotrophic factor (e.g. pain of inflammation, kidney, lung,
CC   cardiovascular or psychiatric disorders and some sorts of tumours)
XX
SQ   Sequence 830 AA;

  Query Match             98.7%;  Score 4436.5;  DB 2;  Length 830;
  Best Local Similarity   98.9%;  Pred. No. 0;
  Matches  830;  Conservative    0;  Mismatches    0;  Indels    9;  Gaps    1;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              |||||||||||||||||||||||||||||||||||||||||         ||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFP---------DEVSPTPPIT 411

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 471

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 531

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 591

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 651

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 711
```

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Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 771

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        772 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 830


RESULT 7
AAR81631
ID   AAR81631 standard; protein; 825 AA.
XX
AC   AAR81631;
XX
DT   08-JUL-1996  (first entry)
XX
DE   Human trkC receptor protein mutant.
XX
KW   trkC receptor; tyrosine-kinase; enzyme; protease; inflammation; pain;
KW   diagnosis; neurotrophic factor; kidney; lung; psychiatric disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 72. .75
FT                   /note= "potential N-linked glycosylation site"
FT   Misc-difference 79. .82
FT                   /note= "potential N-linked glycosylation site"
FT   Misc-difference 133. .136
FT                   /note= "potential N-linked glycoylation site"
FT   Misc-difference 163. .166
FT                   /note= "potential N-linked glycosylation site"
FT   Misc-difference 203. .206
FT                   /note= "potential N-linked glycoylation site"
FT   Misc-difference 218. .221
FT                   /note= "potential N-linked glycosylation site"
FT   Misc-difference 232. .235
FT                   /note= "potential N-linked glycosylation site"
FT   Misc-difference 259. .262
FT                   /note= "potential N-linked glycosylation site"
FT   Misc-difference 267. .270
FT                   /note= "potential N-linked glycosylation site"
FT   Misc-difference 272. .275
FT                   /note= "potential N-linked glycosylation site"
FT   Misc-difference 294. .297
FT                   /note= "potential N-linked glycosylation site"
FT   Misc-difference 375. .378
FT                   /note= "potential N-linked glycosylation site"
FT   Misc-difference 388. .391
FT                   /note= "potential N-linked glycosylation site"
FT   Domain          430. .453
FT                   /note= "transmembrane domain"
FT   Misc-difference 529
FT                   /note= "splice site resulting in truncated form"
FT   Domain          544. .824
FT                   /note= "tyrosine-kinase domain"
XX
PN   WO9525795-A1.
XX
PD   28-SEP-1995.
XX
PF   17-MAR-1995;   95WO-US003426.
XX
PR   18-MAR-1994;   94US-00215139.
PR   05-AUG-1994;   94US-00286846.
PR   20-DEC-1994;   94US-00359705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Presta LG,  Shelton DL,  Urfer R;
XX
DR   WPI; 1995-344616/44.
XX
PT   New human trkB and trkC poly:peptide(s) and fusion proteins contg. them -
PT   also DNA, vectors and transformed cells useful in treatment and diagnosis
PT   of abnormal neurotrophic factor expression, e.g. inflammatory pain.
XX
PS   Claim 16; Fig 2A; 117pp; English.
XX
CC   This DNA sequence may be expressed recombinantly for the production of
CC   human trkC receptor, and to detect or amplify trkC genes. The encoded
CC   protein may be used as a reagent in kinase receptor activation assays,
CC   and therapeutically in diseases associated with over or under expression
CC   of neurotrophic factor (e.g. pain of inflammation, kidney, lung,
CC   cardiovascular or psychiatric disorders and some sorts of tumours)
XX
SQ   Sequence 825 AA;

  Query Match            97.6%;  Score 4391;  DB 2;  Length 825;
  Best Local Similarity  98.3%;  Pred. No. 0;
  Matches  825;  Conservative    0;  Mismatches    0;  Indels   14;  Gaps    1;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR--------- 711

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 -----VGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 766
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Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 825


RESULT 8
AAY06595
ID   AAY06595 standard; protein; 825 AA.
XX
AC   AAY06595;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Neurotrophin-3 receptor TrkC.
XX
KW   Neurotrophin-3; NT-3; human; TrkC; receptor; apoptosis; medulloblastoma;
KW   brain tumour; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO9940103-A1.
XX
PD   12-AUG-1999.
XX
PF   10-FEB-1999;   99WO-US002871.
XX
PR   10-FEB-1998;   98US-00074176.
XX
PA   (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI   Pomeroy SL,  Segal RA;
XX
DR   WPI; 1999-494270/41.
DR   N-PSDB; AAX87599.
XX
PT   Analyzing a medulloblastoma by correlation of expression levels of the
PT   neurotrophin-3 receptor TrkC.
XX
PS   Disclosure; Page 49-51; 52pp; English.
XX
CC   This protein comprises TrkC, the specific receptor of neurotropin-3 (NT-
CC   3, see AAY06594). The invention relates to the discovery that nearly all
CC   medulloblastomas express NT-3 and TrkC. NT-3 promotes apoptosis in some
CC   medulloblastomas. High levels of TrkC expression correlate with a
CC   favorable prognosis. The invention provides methods for analyzing a
CC   medulloblastoma, a kit for assaying a medulloblastoma, a method of
CC   screening candidate substances for their potential activity as
CC   therapeutics of medulloblastoma, and a method for treating a
CC   medulloblastoma. Treatment may involve administering NT-3, an NT-3
CC   agonist or an NT-3 modulator directly to the central nervous system of a
CC   patient. Alternatively, an NT-3 nucleic acid can be delivered near or
CC   directly to the medulloblastoma. Treatment can be supplemented by the
CC   additional step of raising levels of TrkC expression in a medulloblastoma
CC   by administering a TrkC-encoding nucleic acid
XX
SQ   Sequence 825 AA;

  Query Match           97.4%;  Score 4381;  DB 2;  Length 825;
  Best Local Similarity  98.1%;  Pred. No. 0;
  Matches  823;  Conservative    2;  Mismatches    0;  Indels   14;  Gaps    1;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPNAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR--------- 711

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 -----VGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 766

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 825


RESULT 9
AAM50852
ID   AAM50852 standard; protein; 864 AA.
XX
AC   AAM50852;
XX
DT   01-MAY-2002  (first entry)
XX
DE   Rat receptor tyrosine kinase TrkC.
XX
KW   Receptor tyrosine kinase; TrkC; receptor; rat; neurotrophin-3;
KW   Huntington's disease; Parkinson's disease; Alzheimer's disease;
KW   amyotrophic lateral sclerosis; neurodegenerative disease; cancer;
KW   neuroprotective; nootropic; anticonvulsant; antiparkinsonian; enzyme;
KW   cytostatic; therapy.
XX
OS   Rattus norvegicus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .31
FT                   /label= Signal_peptide
FT   Protein         32. .864
FT                   /label= Mature_protein
FT   Domain          32. .429
FT                   /label= Extracellular
FT   Modified-site   68
FT                   /note= "N-glycosylated"
FT   Modified-site   72
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```
FT                   /note= "N-glycosylated"
FT   Modified-site   79
FT                   /note= "N-glycosylated"
FT   Modified-site   133
FT                   /note= "N-glycosylated"
FT   Modified-site   163
FT                   /note= "N-glycosylated"
FT   Modified-site   203
FT                   /note= "N-glycosylated"
FT   Modified-site   218
FT                   /note= "N-glycosylated"
FT   Domain          227. .288
FT                   /label= Ig-like_C2-type
FT   Modified-site   232
FT                   /note= "N-glycosylated"
FT   Modified-site   259
FT                   /note= "N-glycosylated"
FT   Modified-site   267
FT                   /note= "N-glycosylated"
FT   Modified-site   272
FT                   /note= "N-glycosylated"
FT   Modified-site   294
FT                   /note= "N-glycosylated"
FT   Domain          319. .382
FT                   /label= Ig-like_C2-type
FT   Modified-site   375
FT                   /note= "N-glycosylated"
FT   Modified-site   388
FT                   /note= "N-glycosylated"
FT   Domain          430. .453
FT                   /label= Transmembrane
FT   Domain          454. .864
FT                   /label= Cytoplasmic
FT   Binding-site    516
FT                   /note= "interaction with SHC protein"
FT   Modified-site   516
FT                   /note= "O-phosphorylated"
FT   Misc-difference 529. .612
FT                   /note= "replaced by WVFSNIDNHGILNLKDNRDHLVPSTHYIYEE
FT                   PEVQSGDVSYPRSHGFREIMLNPISLSGHSKPLNHGIYVEDVN VYFSKGRHGF in
FT                   isoform IC158/TRKCTK-"
FT   Misc-difference 529. .597
FT                   /note= "replaced by WVFSNIDNHGILNLKDNRDHLVPSTHYIYEE
FT                   PEVQSGDVSYPRSHGELLPLTSLYEVKPLPLPVLILKT in isoform IC143"
FT   Misc-difference 529. .567
FT                   /note= "replaced by CFREIMLNPISLSGHSKPLNHGIYVEDVNVY
FT                   FSKGRHGF in isoform IC113"
FT   Misc-difference 529. .562
FT                   /note= "replaced by FGRIEGFAYGKRYVVMTSVHCHPCWFRFG GLEWL
FT                   in isoform IC108"
FT   Domain          538. .853
FT                   /label= Protein_kinase
FT   Region          544. .552
FT                   /note= "ATP binding site"
FT   Misc-difference 563. .864
FT                   /note= "missing in isoform IC108"
FT   Misc-difference 568. .864
FT                   /note= "missing in isoform IC113"
FT   Region          572
FT                   /note= "ATP binding site"
FT   Misc-difference 598. .864
FT                   /note= "missing in isoform IC143"
FT   Misc-difference 613. .864
FT                   /note= "missing in isoform IC158"
FT   Active-site     679
FT   Modified-site   705
FT                   /note= "O-phosphorylated"
FT   Modified-site   709
FT                   /note= "O-phosphorylated"
FT   Modified-site   710
FT                   /note= "O-phosphorylated"
FT   Misc-difference 712. .736
FT                   /note= "missing in isoform TrkC-14/KI14"
FT   Misc-difference 732. .750
FT                   /note= "missing in isoform TrkC"
FT   Misc-difference 737. .750
FT                   /note= "missing in isoform TrkC-25"
FT   Binding-site    859
FT                   /note= "interaction with PLC-gamma-1"
FT   Modified-site   859
FT                   /note= "O-phosphorylated"
XX
PN   WO200203071-A2.
XX
PD   10-JAN-2002.
XX
PF   05-JUL-2001; 2001WO-US021472.
XX
PR   05-JUL-2000; 2000US-0215778P.
XX
PA   (PANG-) PANGENE CORP.
XX
PI   Bates AT;
XX
DR   WPI; 2002-179638/23.
XX
PT   Screening for a neurotrophic factor mimetic, useful for treating, e.g.,
PT   cancer and Alzheimer's, comprises combining a candidate mimetic with a
PT   fragment of a tyrosine kinase protein.
XX
PS   Disclosure; Fig 12A; 107pp; English.
XX
CC   The present sequence is that of rat receptor tyrosine kinase TrkC, the
CC   receptor for neurotrophin-3 (NT-3). The invention concerns Trks and their
CC   ligands that modulate cell growth, differentiation and survival. Trk
CC   proteins are known to mediate the activities of neurotrophins and are
CC   also known proto-oncogenes. Methods are claimed for screening for small
CC   molecule neurotrophic factor (NTF) mimetics, such as the cyclic peptide
CC   given in AAM50844, capable of binding to a Trk protein or of modulating
CC   the binding of a neurotrophin to a Trk protein. Also claimed are
CC   medicaments comprising a small molecule NTF mimetic and their use in
CC   claimed methods for treatment of cancer or a neurodegenerative disease
CC   selected from Huntington's disease, Parkinson's disease, Alzheimer's
CC   disease and amyotrophic lateral sclerosis
XX
SQ   Sequence 864 AA;

  Query Match             96.9%;  Score 4358.5;  DB 5;  Length 864;
  Best Local Similarity   94.3%;  Pred. No. 0;
  Matches  815;  Conservative   14;  Mismatches   10;  Indels   25;  Gaps    1;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:|||||||||||||||||| ||||||||||||||||||||||:|||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRGLHTLNAVDMELYTGLQKLTIKNSGLRNIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              :|:||:||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RLDSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              |||||||||| |||:|||||||||||||| |||||:|||||||||||::|||||:||
Db        301 VYYPPRVVSLVEPEVRLEHCIEFVVRGNPTPTLHWLYNGQPLRESKIIHMDYYQEGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
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                ||||||||||||||||||||| |||||||||||||||||||||| |    : |||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNALGTANQTINGHFLKEPFPESTDFFDFESDASPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
                |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR--------- 711
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYREGPYQKGPF 720

Qy        712 ----------------LFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWS 755
                              ||||||||||||||||||||||||||||||||||||||||||||
Db        721 SVSWQQQRLAASAASTLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWS 780

Qy        756 FGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRL 815
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 FGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRL 840

Qy        816 NIKEIYKILHALGKATPIYLDILG 839
                |||||||||||||||||||||||
Db        841 NIKEIYKILHALGKATPIYLDILG 864
```

RESULT 10
AAU81284
ID AAU81284 standard; protein; 808 AA.
XX
AC AAU81284;
XX
DT 09-APR-2002 (first entry)
XX
DE Human trkC receptor.
XX
KW Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;
KW trkA; trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;
KW peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;
KW large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;
KW nerve cell injury; blood cell disorder; leukopaenia; eosinopaenia; wound;
KW basopaenia; lymphopaenia; monocytopaenia; neutropaenia; cancer; ulcer;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
KW sickle cell disease; cardiac ischaemia; cerebrovascular disorder;
KW cellular degeneration; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200198361-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020153.
XX
PR 22-JUN-2000; 2000US-0213141P.
PR 05-OCT-2000; 2000US-0238319P.
XX
PA (GETH) GENENTECH INC.
XX
PI Devaux B, Hongo JS, Presta LG, Shelton DL;
XX
DR WPI; 2002-130790/17.
DR N-PSDB; ABK24399.
XX
PT Novel anti-trkC agonist monoclonal antibody useful for treating
PT neurodegenerative disease, shows no significant cross-reactivity with
PT trkA/trkB, and recognizes epitope in domain 5 of trkC.
XX
PS Disclosure; Fig 20; 121pp; English.
XX
CC The invention relates to an anti-trkC agonist monoclonal antibody which
CC shows no significant cross-reactivity with trkA or trkB, and recognizes
CC an epitope in domain 5 of trkC. The antibodies of the invention are
CC effective in the treatment of cisplatin- or pyridoxine-induced
CC neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre
CC sensory neuropathy, neurodegenerative disease including amyotrophic
CC lateral sclerosis, nerve cell injuries, disorders of insufficient blood
CC cells such as leukopaenia including eosinopaenia, basopaenia,
CC lymphopaenia, monocytopaenia, neutropaenia, Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and tumours. The sequences are
CC also useful for inducing angiogenesis for treating wounds, ulcers and
CC diabetic complications of sickle cell disease, for treating cardiac
CC ischaemia and cerebrovascular disorders and in the diagnosis of diseases
CC involving cellular degeneration. Sequences AAU81229-AAU81284 represent
CC human and mouse anti-trkC agonist monoclonal antibodies and antibody
CC fragments of the invention
XX
SQ Sequence 808 AA;

```
  Query Match             96.2%;  Score 4328;  DB 5;  Length 808;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  808;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         32 CPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENWRSL 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENWRSL 60

Qy         92 HTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQTLS 151
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQTLS 120

Qy        152 LRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCDLPE 211
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCDLPE 180

Qy        212 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 271
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 240

Qy        272 NVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPP 331
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPP 300

Qy        332 TLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTI 391
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTI 360

Qy        392 NGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFV 451
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFV 420

Qy        452 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 511
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 480

Qy        512 ENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAV 571
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAV 540

Qy        572 KALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRA 631
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRA 600

Qy        632 HGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANL 691
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 HGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANL 660
```

```
Qy        692 LVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTES 751
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTES 720

Qy        752 DVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREP 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 DVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREP 780

Qy        812 QQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||
Db        781 QQRLNIKEIYKILHALGKATPIYLDILG 808
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RESULT 11
AAR71621
ID   AAR71621 standard; protein; 839 AA.
XX
AC   AAR71621;
XX
DT   25-MAR-2003  (revised)
DT   04-MAY-1995  (first entry)
XX
DE   Porcine TrkC K2 isoform protein.
XX
KW   Porcine; TrkC; cell surface; receptor; tyrosine kinase; transmembrane;
KW   Trk; murine; expression; vector; pMEX-neo; oncogene; proto-oncogene;
KW   oncogenesis; anticancer agent.
XX
OS   Sus scrofa.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .31
FT                   /label= signal peptide
FT   Domain          32. .429
FT                   /label= extracellular domain
FT   Modified-site   68. .70
FT                   /label= N-linked glycosylation
FT   Modified-site   72. .74
FT                   /label= N-linked glycosylation
FT   Modified-site   79. .81
FT                   /label= N-linked glycosylation
FT   Modified-site   133. .135
FT                   /label= N-linked glycosylation
FT   Modified-site   163. .165
FT                   /label= N-linked glycosylation
FT   Modified-site   203. .205
FT                   /label= N-linked glycosylation
FT   Modified-site   218. .220
FT                   /label= N-linked glycosylation
FT   Modified-site   232. .234
FT                   /label= N-linked glycosylation
FT   Modified-site   259. .261
FT                   /label= N-linked glycosylation
FT   Modified-site   267. .269
FT                   /label= N-linked glycosylation
FT   Modified-site   272. .274
FT                   /label= N-linked glycosylation
FT   Modified-site   294. .296
FT                   /label= N-linked glycosylation
FT   Modified-site   375. .377
FT                   /label= N-linked glycosylation
FT   Modified-site   388. .390
FT                   /label= N-linked glycosylation
FT   Domain          430. .453
FT                   /label= transmembrane domain
FT   Domain          454. .839
FT                   /label= intracellular domain
FT   Domain          544. .825
FT                   /label= kinase catalytic domain
FT   Domain          545. .572
FT                   /label= ATP binding domain
FT   misc_feature    711. .725
FT                   /note= "deduced a.a. sequence not found in specification.
FT                   Extra 14 amino acids found in the tyrosine kinase
FT                   catalytic domain of porcine variant TrkC K2. This is due
FT                   to an extra 42 bases found in the TrkC K2 DNA sequence
FT                   between bases 2164-5 of the porcine TrkC K1 gene
FT                   sequence"
XX
PN   US5348856-A.
XX
PD   20-SEP-1994.
XX
PF   07-JUL-1992;   92US-00912952.
XX
PR   08-JUL-1991;   91US-00726466.
XX
PA   (SQUI ) SQUIBB & SONS INC E R.
XX
PI   Lamballe F,  Barbacid M;
XX
DR   WPI; 1994-302202/37.
DR   N-PSDB; AAQ69036.
XX
PT   New nucleic acid encoding trkC protein and related vectors - and
PT   transformed cells, useful for studying onco:genesis and identifying
PT   anticancer agents.
XX
PS   Example 2; Col 17; 29pp; English.
XX
CC   This is the amino acid sequence of porcine TrkC K2, an isoform of the
CC   TrkC K1 gene (AAQ69029). The variant contains an additional 42 bases in
CC   the tyrosine kinase region of the gene, at position 2164-2206. This
CC   produces a lengthened protein, with an extra 14 amino acids (711-725),
CC   which retains activity. The gene was obtained from an adult porcine brain
CC   cDNA library. The TrkC genes are members of a family of cell surface
CC   receptors with tyrosine kinase activity. The porcine protein contains a
CC   signal region, a transmembrane region and a tyrosine kinase region. The
CC   protein also contains many putative sites for N-glucosylation. Porcine
CC   and murine adult brain libraries were screened for isoforms of TrkC.
CC   Several clones were obtained; porcine TrkC K2 and NC1, murine TrkC K3 and
CC   NC2. The isoforms (AAQ69033-36) either contain altered or shortened
CC   sequences in the protein as compared to their natural forms. The clone of
CC   the porcine TrkC gene was cloned into the mammalian expression vector
CC   pMEX-neo to form pFL20. Cells transformed with the expression plasmid can
CC   be used to produce TrkC protein. This can provide the basis for
CC   generating specific antibodies to TrkC protein useful for the detection
CC   of TrkC protein in immunoassays. The TrkC gene is related to the trk
CC   oncogene and can used in the study of the role of trkC in oncogenesis,
CC   especially in the detection of potential anticancer agents. (Updated on
CC   25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 839 AA;
```

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  Query Match             95.6%;  Score 4299;  DB 2;  Length 839;
  Best Local Similarity   95.8%;  Pred. No. 0;
  Matches  806;  Conservative   11;  Mismatches   20;  Indels    4;  Gaps    2;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:|||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRGLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              |||||:||||:|||||||||||||||||||||||||||||||||||:||||||||||||
Db        181 KLNSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVVTCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
```

```
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Db        301 VHYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKITHVEYYQEGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Db        361 GCLLFNKPTHYNNGNYTLNRQEPLGTANQTINGHFLKEPFPESTDNFVSFYEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHIN--HGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538

Db        481 LHHDQPWHHHTLITGRRAGHS--VIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538

Qy        539 VLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598

Db        539 VLKRELGEGAFGKVFLAECYNLSPTKVKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598

Qy        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658

Db        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658

Qy        659 IASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGN 718

Db        659 IASQICSGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGN 718

Qy        719 DFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 778

Db        719 DFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 778

Qy        779 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 838

Db        779 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 838

Qy        839 G 839

Db        839 G 839
```

```
RESULT 12
AAW11942
ID   AAW11942 standard; protein; 850 AA.
XX
AC   AAW11942;
XX
DT   16-OCT-2003  (revised)
DT   27-AUG-2003  (revised)
DT   30-APR-1997  (first entry)
XX
DE   gD.trkC fusion useful in kinase receptor activation assay.
XX
KW   Kinase receptor activation; KIRA; receptor protein tyrosine kinase; rPTK;
KW   signal transduction; autophosphorylation; gD.trkC;
KW   enzyme-linked immunosorbent assay; ELISA.
XX
OS   Human herpesvirus 1.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .29
FT                   /label= gD
FT                   /note= "herpes simplex virus glycoprotein D polypeptide
FT                   flag"
FT   Peptide         30. .56
FT                   /label= Sig_peptide
FT                   /note= "trkC signal peptide"
FT   Protein         57. .850
FT                   /label= Mat_protein
FT                   /note= "trkC mature protein"
XX
PN   WO9514930-A1.
XX
PD   01-JUN-1995.
XX
PF   18-NOV-1994;   94WO-US013329.
XX
PR   23-NOV-1993;   93US-00157563.
PR   20-DEC-1993;   93US-00170558.
PR   05-AUG-1994;   94US-00286305.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Godowski PJ,  Mark MR,  Sadick MD,  Wong WLT;
XX
DR   WPI; 1995-207042/27.
DR   N-PSDB; AAT51458.
XX
PT   Measuring auto-phosphorylation of tyrosine kinase receptor - to identify
PT   and characterise potential (ant)agonists of TKR.
XX
PS   Example 3; Fig 14a-g; 148pp; English.
XX
CC   Fusion proteins gD.trkA (AAW11940) gD.trkB (AAW11941) and gD.trkC
CC   (AAW11942) respectively comprise human receptor protein tyrosine kinases
CC   (rPTKs) trkA, B and C fused at their N-terminal ends to a herpes simplex
CC   virus glycoprotein D polypeptide flag. They can be expressed in e.g.
CC   dp12.CHO host cells using DNA constructs (AAT51456- 58) that include the
CC   gd.trk gene fusions. gD.trkA, B and C are used in kinase receptor
CC   activation, enzyme-linked immunosorbent assays (KIRA ELISA) to measure
CC   autophosphorylation of rPTK kinase domains. These assays are used to
CC   identify and characterise potential (ant)agonists of rPTKs, study ligand-
CC   receptor interactions, measure phosphatase activity and identify rPTK
CC   ligands in clinical samples. (Updated on 27-AUG-2003 to correct OS
CC   field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 850 AA;
```

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  Query Match             93.9%;  Score 4222;  DB 2;  Length 850;
  Best Local Similarity   98.3%;  Pred. No. 0;
  Matches  794;  Conservative    0;  Mismatches    0;  Indels   14;  Gaps    1;

Qy         32 CPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENWRSL 91

Db         57 CPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENWRSL 116

Qy         92 HTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQTLS 151

Db        117 HTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQTLS 176

Qy        152 LRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCDLPE 211

Db        177 LRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCDLPE 236

Qy        212 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 271

Db        237 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 296

Qy        272 NVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPP 331

Db        297 NVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPP 356

Qy        332 TLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTI 391

Db        357 TLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTI 416

Qy        392 NGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFV 451

Db        417 NGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFV 476

Qy        452 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 511
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 536

Qy        512 ENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAV 571
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 ENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAV 596

Qy        572 KALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRA 631
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 KALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRA 656

Qy        632 HGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANL 691
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 HGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANL 716

Qy        692 LVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTES 751
                |||||||||||||||||||              ||||||||||||||||||||||||||
Db        717 LVKIGDFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTES 762

Qy        752 DVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREP 811
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 DVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREP 822

Qy        812 QQRLNIKEIYKILHALGKATPIYLDILG 839
                |||||||||||||||||||||||||||
Db        823 QQRLNIKEIYKILHALGKATPIYLDILG 850
```

RESULT 13
AAR62021
ID AAR62021 standard; protein; 825 AA.
XX
AC AAR62021;
XX
DT 25-MAR-2003 (revised)
DT 28-APR-1995 (first entry)
XX
DE Porcine TrkC protein.
XX
KW Porcine; TrkC; cell surface; receptor; tyrosine kinase; transmembrane;
KW Trk; murine; expression; vector; pMEX-neo; oncogene; proto-oncogene;
KW oncogenesis; anticancer agent.
XX
OS Sus scrofa.
XX

FH	Key	Location/Qualifiers
FT	Domain	1. .31
FT		/label= signal peptide
FT	Domain	32. .429
FT		/label= extracellular domain
FT	Modified-site	68. .70
FT		/label= N-linked glycosylation
FT	Modified-site	72. .74
FT		/label= N-linked glycosylation
FT	Modified-site	79. .81
FT		/label= N-linked glycosylation
FT	Modified-site	133. .135
FT		/label= N-linked glycosylation
FT	Modified-site	163. .165
FT		/label= N-linked glycosylation
FT	Modified-site	203. .205
FT		/label= N-linked glycosylation
FT	Modified-site	218. .220
FT		/label= N-linked glycosylation
FT	Modified-site	232. .234
FT		/label= N-linked glycosylation
FT	Modified-site	259. .261
FT		/label= N-linked glycosylation
FT	Modified-site	267. .269
FT		/label= N-linked glycosylation
FT	Modified-site	272. .274
FT		/label= N-linked glycosylation
FT	Modified-site	294. .296
FT		/label= N-linked glycosylation
FT	Modified-site	375. .377
FT		/label= N-linked glycosylation
FT	Modified-site	388. .390
FT		/label= N-linked glycosylation
FT	Domain	430. .453
FT		/label= transmembrane domain
FT	Domain	454. .825
FT		/label= intracellular domain
FT	Domain	544. .810
FT		/label= kinase catalytic domain
FT	Domain	545. .572
FT		/label= ATP binding domain

XX
PN US5348856-A.
XX
PD 20-SEP-1994.
XX
PF 07-JUL-1992; 92US-00912952.
XX
PR 08-JUL-1991; 91US-00726466.
XX
PA (SQUI) SQUIBB & SONS INC E R.
XX
PI Lamballe F, Barbacid M;
XX
DR WPI; 1994-302202/37.
DR N-PSDB; AAQ69029.
XX
PT New nucleic acid encoding trkC protein and related vectors - and
PT transformed cells, useful for studying onco:genesis and identifying
PT anticancer agents.
XX
PS Claim 4; Fig 1; 29pp; English.
XX
CC This is the amino acid sequence of the gene for porcine TrkC, a family of
CC cell surface receptors with tyrosine kinase activity. The protein
CC contains a signal region, a transmembrane region and a tyrosine kinase
CC region. The protein also contains many putative sites for N-
CC glucosylation. The gene was obtained from adult porcine brain cDNA
CC library with a fragment of pDM17 encoding the entire human Trk catalytic
CC region. The complete gene isolated by rescreening the library under
CC stringent conditions with a fragment from the 3' region. A 2.2 kb
CC fragment was cloned into pBluescript and called pFL15. Porcine and murine
CC adult brain libraries were screened for isoforms of Trk. Several clones
CC were obtained; porcine TrkC K2 and NC1, murine TrkC K3 and NC2. The
CC isoforms (AAQ69033-36) either contain altered or shortened sequences in
CC the protein as compared to their natural forms. The clone of the porcine
CC TrkC gene was cloned into the mammalian expression vector pMEX-neo to
CC form pFL20. Cells transformed with the expression plasmid can be used to
CC produce TrkC protein. This can provide the basis for generating specific
CC antibodies to TrkC protein useful for the detection of TrKc protein in
CC immunoassays. The TrkC gene is related to the trk oncogene and can used
CC in the study of the role of trkC in oncogenesis, especially in the
CC detection of potential anticancer agents. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
SQ Sequence 825 AA;

Query Match 93.2%; Score 4193; DB 2; Length 825;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 792; Conservative 11; Mismatches 20; Indels 18; Gaps 3;

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Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRGLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
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```
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              |||||:||||:||||||||||||||||||||||||||||||||||||:||||||||||||
Db        181 KLNSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVVTCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              |:|||||||||||||||||||||||||||||||||||||||||||| |||||||||:||
Db        301 VHYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKITHVEYYQEGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              |||||||||||||||||  : |||||||||||||||||||||||: | |||||||||
Db        361 GCLLFNKPTHYNNGNYTLNRQEPLGTANQTINGHFLKEPFPESTDNFVSFYEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHIN--HGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538
              |||    |  |  :   ||    |||||||||||||||||||||||||||||||||||
Db        481 LHHDQPWHHHTLITGRRAGHS--VIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538

Qy        539 VLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        539 VLKRELGEGAFGKVFLAECYNLSPTKVKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598

Qy        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658

Qy        659 IASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGN 718
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 IASQICSGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR------- 711

Qy        719 DFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 778
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 -------VGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 764

Qy        779 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 824

Qy        839 G 839
              |
Db        825 G 825
```

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RESULT 14
AAR27148
ID   AAR27148 standard; protein; 825 AA.
XX
AC   AAR27148;
XX
DT   25-MAR-2003  (revised)
DT   20-MAY-1998  (first entry)
XX
DE   Adult porcine trkC proto-oncogene product.
XX
KW   pig; pork; antagonist; agonist; neurotropic factor; tyrosine kinases;
KW   nerve growth factor; neuronal death; degenerative neural diseases;
KW   Alzheimers; Parkinsons; anticancer drugs; ss.
XX
OS   Sus scrofa domestica.
XX
FH   Key             Location/Qualifiers
FT   peptide         1. .31
FT                   /note= "signal peptide"
FT   region          32. .429
FT                   /note= "extracellular region encompasses 14 consensus N-
FT                   glycosylation sites"
FT   region          430. .453
FT                   /note= "transmembrane domain"
FT   region          454. .825
FT                   /note= "cytoplasmic region"
FT   domain          544. .810
FT                   /note= "kinase catalytic domain"
FT   binding_site    545. .572
FT                   /note= "consensus sequence for ATP binding motif"
XX
PN   EP504914-A2.
XX
PD   23-SEP-1992.
XX
PF   20-MAR-1992;   92EP-00104872.
XX
PR   21-MAR-1991;   91US-00674285.
PR   08-JUL-1991;   91US-00725332.
PR   25-FEB-1992;   92US-00837814.
XX
PA   (SQUI ) SQUIBB & SONS INC E R.
XX
PI   Barbacid M,  Klein R;
XX
DR   WPI; 1992-317823/39.
DR   N-PSDB; AAQ28668.
XX
PT   Detection of agonists and antagonists of neurotrophic factors - using
PT   protein prods. of the TRK family of proto-oncogene(s).
XX
PS   Example 4; Page 47; 98pp; English.
XX
CC   This sequences represents the porcine trk proto-oncogene gene product. It
CC   was deduced from the cDNA sequence AAQ28668. It has a calculated
CC   molecular weight of 93,129Da and exhibits the characteristic features of
CC   cell surface tyrosine protein kinase including a signal peptide, a long
CC   extracellular region encompassing 14 consensus N-glycosylation sites (Asn
CC   -X-Ser-Thr, posns. 32 to 429), a single transmembrane domain (430 to 453)
CC   and a cytoplasmic region (454 to 825) including the kinase catalytic
CC   domain (544 to 810). The concensus sequence for the ATP binding motif is
CC   present at 545 to 572. Like the other two members of the trk gene family
CC   has a very short carboxy terminal region of 15 amino acids including a
CC   conserved free tyrosine at the carboxy terminus. Overall homology to
CC   human trk and mouse trkB is 67% and 68% respectively. Their external
CC   domains exhibit 54% and 53% similarities. The twelve external cysteine
CC   residues of trrkC are present in the corresponding regions of trkB, and
CC   ten of them are shared with trk. There is also present a highly conserved
CC   region which depicts an 82% identity among the three kinases, which is
CC   also part of the 51 amino acid deletion responsible for the activation of
CC   the trk5 oncogene. The catalytic domain is 76% identical to that of human
CC   trk and 83% to that of mouse trkB. Protein products of the trk family of
CC   proto- oncogenes allow a highly specific detection of neurotrophic
CC   factors, eg. nerve growth factor, or their antagonists or agonists.
CC   Agonists thus identified could prove useful to avoid neuronal death and
CC   in the treatment of degenerative neural diseases eg. Alzheimers or
CC   Parkinsons. Antagonists may be potential anticancer drugs. The trk family
CC   of tyrosine kinases mediate the biological activities of the neurotrophic
CC   factors. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 825 AA;
```

```
  Query Match             93.2%;  Score 4190;  DB 2;  Length 825;
  Best Local Similarity   94.1%;  Pred. No. 0;
  Matches  791;  Conservative   12;  Mismatches   20;  Indels   18;  Gaps    3;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:|||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRGLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
```

```
Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              |||||:||||:|||||||||||||||||||||||||||||||||||:||||||||||||
Db        181 KLNSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVVTCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        301 VHYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKITHVEYYQEGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||  : |||||||||||||||||||||: | |||||||||
Db        361 GCLLFNKPTHYNNGNYTLNRQEPLGTANQTINGHFLKEPFPESTDNFVSFYEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHIN--HGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538
              |||    |  |  :   ||    ||||||||||||||||||||||||||||||||||||
Db        481 LHHDQPWHHHTLITGRRAGHS--VIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538

Qy        539 VLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        539 VLKRELGEGAFGKVFLAECYNLSPTKVKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598

Qy        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658

Qy        659 IASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGN 718
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 IASQICSGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR------- 711

Qy        719 DFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 778
                    ||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        712 -------VGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWDIFTYGKQPWFQLSNTE 764

Qy        779 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 824

Qy        839 G 839
              |
Db        825 G 825
```

RESULT 15
AAR30883
ID AAR30883 standard; protein; 825 AA.
XX
AC AAR30883;
XX
DT 25-MAR-2003 (revised)
DT 07-MAY-1993 (first entry)
XX
DE trkC gene prod.
XX
KW Oncogenesis; porcine; anti cancer; probe.
XX
OS Sus scrofa.
XX
FH Key   Location/Qualifiers
FT Peptide   1. .31
FT   /note= "signal peptide"
FT Protein   32. .825
FT   /note= "mature"
FT Modified-site   68. .70
FT   /note= "N-glycosylation site"
FT Modified-site   72. .74
FT   /note= "N-glycosylation site"
FT Modified-site   79. .81
FT   /note= "N-glycosylation site"
FT Modified-site   133. .135
FT   /note= "N-glycosylation site"
FT Modified-site   163. .165
FT   /note= "N-glycosylation site"
FT Modified-site   203. .205
FT   /note= "N-glycosylation site"
FT Modified-site   218. .220
FT   /note= "N-glycosylation site"
FT Modified-site   232. .234
FT   /note= "N-glycosylation site"
FT Modified-site   259. .261
FT   /note= "N-glycosylation site"
FT Modified-site   267. .269
FT   /note= "N-glycosylation site"
FT Modified-site   272. .274
FT   /note= "N-glycosylation site"
FT Modified-site   294. .296
FT   /note= "N-glycosylation site"
FT Modified-site   375. .377
FT   /note= "N-glycosylation site"
FT Modified-site   388. .390
FT   /note= "N-glycosylation site"
FT Domain   430. .453
FT   /note= "transmembrane domain"
FT Active-site   544. .810
FT   /note= "tyrosine kinase catalytic domain"
XX
PN EP522530-A2.
XX
PD 13-JAN-1993.
XX
PF 08-JUL-1992; 92EP-00111582.
XX
PR 08-JUL-1991; 91US-00726466.
XX
PA (SQUI) SQUIBB & SONS INC E R.
XX
PI Barbacid M, Lamballe F;
XX
DR WPI; 1993-010384/02.
XX
PT Nucleic acid molecule encoding trkC protein - for studying oncogenesis
PT and identifying potential anticancer drugs.
XX
PS Claim 20; Fig 1B; 36pp; English.
XX
CC An adult porcine brain cDNA library was screened with a probe corresp. to
CC the catalytic domain of the human trk proto-oncogene under relaxed
CC hybridisation conditions. Filters contg. positive plaques were hybridised
CC under stringent conditions with probes specific for either trk or trkB
CC sequences in order to identify undesirable clones. Six positive clones
CC which hybridised only weakly with these probes were characterised. The
CC six clones contained overlapping inserts which were found to be related
CC to but distinct from the trk and trkB proto-oncogenes. None of the clones
CC contained sequences coding for the amino terminus of the putative trkC
CC genee prod. A small probe derived from the 5' end of the longest cDNA
CC clone, pFL7, was used to rescreen the porcine cDNA library. Only one
CC recombinant, carrying a 2.2 kb EcoRI insert was identified and used to
CC generate pFL19. The small size of the 3' untranslated region and the lack
CC of a polyadenylation site suggests that pFL19 lacks a fraction of the 3'
CC untranslated region of the trkC transcript. However, the transcript
CC represents a new trk-related gene and may be used as a probe to screen
CC cDNA and genomic DNA libraries for other sequences encoding trkC-like
CC proteins, which may be used to study oncogenesis and identify potential
CC anticancer drugs. See also AAR30884. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX

SQ Sequence 825 AA;

Query Match 93.2%; Score 4190; DB 2; Length 825;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 791; Conservative 12; Mismatches 20; Indels 18; Gaps 3;

```
Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:|||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRGLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              |||||:||||:|||||||||||||||||||||||||||||||||||:||||||||||||
Db        181 KLNSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVVTCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              |:|||||||||||||||||||||||||||||||||||||||||||| |||||||||:||
Db        301 VHYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKITHVEYYQEGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              |||||||||||||||||  : |||||||||||||||||||||: | |||||||||
Db        361 GCLLFNKPTHYNNGNYTLNRQEPLGTANQTINGHFLKEPFPESTDNFVSFYEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHIN--HGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538
              |||    |  |  :  ||    ||||||||||||||||||||||||||||||||||||
Db        481 LHHDQPWHHHTLITGRRAGHS--VIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538

Qy        539 VLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598
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Db        539 VLKRELGEGAFGKVFLAECYNLSPTKVKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598

Qy        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658
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Db        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658

Qy        659 IASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGN 718
              ||||| ||||||||||||||||||||||||||||||||||||||||||
Db        659 IASQICSGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR------- 711

Qy        719 DFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 778
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Db        712 -------VGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWDIFTYGKQPWFQLSNTE 764

Qy        779 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 824

Qy        839 G 839
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Db        825 G 825
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Search completed: July 12, 2004, 13:37:18
Job time : 65 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:36:10 ; Search time 23 Seconds
(without alignments)
1883.226 Million cell updates/sec

Title: US-09-966-147-6
Perfect score: 4497
Sequence: 1 MDVSLCPAKCSFWRIFLLGS.....IYKILHALGKATPIYLDILG 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4497	100.0	839	2	US-08-359-705B-6	Sequence 6, Appli
2	4497	100.0	839	2	US-08-286-846A-6	Sequence 6, Appli
3	4497	100.0	839	2	US-08-457-880A-6	Sequence 6, Appli
4	4497	100.0	839	3	US-08-444-622A-6	Sequence 6, Appli
5	4497	100.0	839	3	US-08-942-562-6	Sequence 6, Appli
6	4497	100.0	839	3	US-09-156-923-6	Sequence 6, Appli
7	4222	93.9	850	1	US-08-286-305A-7	Sequence 7, Appli
8	4222	93.9	850	2	US-08-441-104A-7	Sequence 7, Appli
9	4222	93.9	850	2	US-08-440-816A-7	Sequence 7, Appli
10	4222	93.9	850	3	US-09-417-381A-7	Sequence 7, Appli
11	4172	92.8	825	1	US-07-912-952-2	Sequence 2, Appli
12	3673	81.7	728	1	US-07-912-952-4	Sequence 4, Appli
13	2836	63.1	612	2	US-08-359-705B-8	Sequence 8, Appli
14	2836	63.1	612	2	US-08-286-846A-8	Sequence 8, Appli
15	2836	63.1	612	2	US-08-457-880A-8	Sequence 8, Appli
16	2836	63.1	612	3	US-08-444-622A-8	Sequence 8, Appli
17	2836	63.1	612	3	US-08-942-562-8	Sequence 8, Appli
18	2836	63.1	612	3	US-09-156-923-8	Sequence 8, Appli
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20	2277	50.6	822	2	US-08-359-705B-2	Sequence 2, Appli
21	2277	50.6	822	2	US-08-286-846A-2	Sequence 2, Appli
22	2277	50.6	822	2	US-08-457-880A-2	Sequence 2, Appli
23	2277	50.6	822	3	US-08-444-622A-2	Sequence 2, Appli
24	2277	50.6	822	3	US-08-942-562-2	Sequence 2, Appli
25	2277	50.6	822	3	US-09-156-923-2	Sequence 2, Appli
26	2259.5	50.2	847	1	US-08-286-305A-5	Sequence 5, Appli
27	2259.5	50.2	847	2	US-08-441-104A-5	Sequence 5, Appli
28	2259.5	50.2	847	2	US-08-440-816A-5	Sequence 5, Appli
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31	1960	43.6	790	2	US-08-286-846A-9	Sequence 9, Appli
32	1960	43.6	790	2	US-08-457-880A-9	Sequence 9, Appli
33	1960	43.6	790	3	US-08-444-622A-9	Sequence 9, Appli
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36	1956	43.5	814	1	US-08-286-305A-3	Sequence 3, Appli
37	1956	43.5	814	2	US-08-441-104A-3	Sequence 3, Appli
38	1956	43.5	814	2	US-08-440-816A-3	Sequence 3, Appli
39	1956	43.5	814	3	US-09-417-381A-3	Sequence 3, Appli
40	1299.5	28.9	641	4	US-09-167-206-4	Sequence 4, Appli
41	1270.5	28.3	285	2	US-08-469-537A-73	Sequence 73, Appl
42	1225.5	27.3	279	2	US-08-469-537A-51	Sequence 51, Appl
43	1199.5	26.7	310	2	US-08-469-537A-74	Sequence 74, Appl
44	1189.5	26.5	294	2	US-08-701-191A-20	Sequence 20, Appl
45	1189.5	26.5	294	4	US-09-664-526-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-359-705B-6
; Sequence 6, Application US/08359705B
; Patent No. 5844092
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shelton, David L.
; APPLICANT: Urfer, Roman
; TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/359,705B
; FILING DATE: 20-Dec-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286846
; FILING DATE: 08/10/94
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/215139
; FILING DATE: 03/18/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P0873P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 839 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-359-705B-6

Query Match 100.0%; Score 4497; DB 2; Length 839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
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Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
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Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
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Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
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Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
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Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
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Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
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Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
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Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
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Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
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Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
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RESULT 2
US-08-286-846A-6
; Sequence 6, Application US/08286846A
; Patent No. 5877016
;  GENERAL INFORMATION:
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shelton, David L.
;    APPLICANT:  Urfer, Roman
;    TITLE OF INVENTION:  Human trk Receptors and Neurotrophic Factor Inhibitors
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/286,846A
;      FILING DATE:  05-Aug-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, PhD., Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  P0873P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8674
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  839 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-286-846A-6

  Query Match             100.0%;  Score 4497;  DB 2;  Length 839;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
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Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
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Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
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Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
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Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
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Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
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Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
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Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
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Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
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Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
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Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
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Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839


RESULT 3
US-08-457-880A-6
; Sequence 6, Application US/08457880A
; Patent No. 5910574
;  GENERAL INFORMATION:
;    APPLICANT:  Leonard G. Presta
;    APPLICANT:  David L. Shelton
;    APPLICANT:  Roman Urfer
;    TITLE OF INVENTION:  HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,880A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,622
;      FILING DATE:  19-May-1995
;      APPLICATION NUMBER:  08/286846
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, PhD., Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  P0873P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-8674
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  839 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-457-880A-6

  Query Match            100.0%;  Score 4497;  DB 2;  Length 839;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
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Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
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Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
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Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839


RESULT 4
US-08-444-622A-6
; Sequence 6, Application US/08444622A
; Patent No. 6025166
;  GENERAL INFORMATION:
;    APPLICANT:  Leonard G. Presta
;    APPLICANT:  David L. Shelton
;    APPLICANT:  Roman Urfer
;    TITLE OF INVENTION:  HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,622A
;      FILING DATE:  19-May-1995
;      CLASSIFICATION:  424
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/286846
;      FILING DATE:  5
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, PhD., Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  P0873P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-8674
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  839 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-444-622A-6

  Query Match           100.0%;  Score 4497;  DB 3;  Length 839;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
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Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839


RESULT 5
US-08-942-562-6
; Sequence 6, Application US/08942562
; Patent No. 6027927
;  GENERAL INFORMATION:
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shelton, David L.
;    APPLICANT:  Urfer, Roman
;    TITLE OF INVENTION:  Human trk Receptors and Neurotrophic
;    TITLE OF INVENTION:  Factor Inhibitors
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/942,562
;      FILING DATE:  01-OCT-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/444,597
;      FILING DATE:  19-May-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, PhD., Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  P0873P1C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8674
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  839 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-942-562-6

  Query Match           100.0%;  Score 4497;  DB 3;  Length 839;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
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Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
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Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
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Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
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Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
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Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
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Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
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Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
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Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
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Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839


RESULT 6
US-09-156-923-6
; Sequence 6, Application US/09156923
; Patent No. 6153189
;  GENERAL INFORMATION:
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shelton, David L.
;    APPLICANT:  Urfer, Roman
;    TITLE OF INVENTION:  Human trk Receptors and Neurotrophic Factor Inhibitors
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  620 Newport Center Drive 16th Floor
;      CITY:  Newport Beach
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/156,923
;      FILING DATE:  18-SEP-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/359,705
;      FILING DATE:  20-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/286846
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/215139
;      FILING DATE:  18-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Dreger, Ginger
;      REGISTRATION NUMBER:  33,055
;      REFERENCE/DOCKET NUMBER:  GENENT.33CP2C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  949/760-0404
;      TELEFAX:  949/760-9502
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  839 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-156-923-6

  Query Match           100.0%;  Score 4497;  DB 3;  Length 839;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
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Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
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Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
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Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
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Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
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RESULT 7
US-08-286-305A-7
; Sequence 7, Application US/08286305A
; Patent No. 5766863
;  GENERAL INFORMATION:
;    APPLICANT:  Godowski, Paul J.
;    APPLICANT:  Mark, Melanie R.
;    APPLICANT:  Sadick, Michael D.
;    APPLICANT:  Shelton, David L.
;    APPLICANT:  Wong, Wai Lee Tan
;    TITLE OF INVENTION:  KINASE RECEPTOR ACTIVATION ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/286,305A
;      FILING DATE:  05-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/170558
;      FILING DATE:  20-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/157563
;      FILING DATE:  23-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lee, Wendy M.
;      REGISTRATION NUMBER:  00,000
;      REFERENCE/DOCKET NUMBER:  854C1P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1994
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  850 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-286-305A-7

  Query Match             93.9%;  Score 4222;  DB 1;  Length 850;
  Best Local Similarity   98.3%;  Pred. No. 0;
  Matches  794;  Conservative    0;  Mismatches    0;  Indels   14;  Gaps    1;

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Db        177 LRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCDLPE 236

Qy        212 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 271
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Db        237 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 296

Qy        272 NVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPP 331
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Db        297 NVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPP 356

Qy        332 TLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTI 391
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Db        357 TLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTI 416

Qy        392 NGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFV 451
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Db        417 NGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFV 476

Qy        452 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 511
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Db        477 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 536

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Db        537 ENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAV 596

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Db        657 HGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANL 716

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Db        717 LVKIGDFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTES 762

Qy        752 DVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREP 811
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Db        823 QQRLNIKEIYKILHALGKATPIYLDILG 850


RESULT 8
US-08-441-104A-7
; Sequence 7, Application US/08441104A
; Patent No. 5891650
;  GENERAL INFORMATION:
;    APPLICANT:  Godowski, Paul J.
;    APPLICANT:  Mark, Melanie R.
;    APPLICANT:  Sadick, Michael D.
;    APPLICANT:  Shelton, David L.
;    APPLICANT:  Wong, Wai Lee Tan
;    TITLE OF INVENTION:  KINASE RECEPTOR ACTIVATION ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 720 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/441,104A
;      FILING DATE:  15-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/286305
;      FILING DATE:  05-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/170558
;      FILING DATE:  20-DEC-1993
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/157563
;      FILING DATE:  23-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lee, Wendy M.
;      REGISTRATION NUMBER:  00,000
;      REFERENCE/DOCKET NUMBER:  854C1P1C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1994
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  850 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-441-104A-7

  Query Match             93.9%;  Score 4222;  DB 2;  Length 850;
  Best Local Similarity   98.3%;  Pred. No. 0;
  Matches  794;  Conservative    0;  Mismatches    0;  Indels   14;  Gaps    1;

Qy         32 CPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENWRSL 91
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Db         57 CPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENWRSL 116

Qy         92 HTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQTLS 151
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Db        237 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 296

Qy        272 NVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPP 331
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Db        297 NVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPP 356

Qy        332 TLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTI 391
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Db        357 TLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTI 416

Qy        392 NGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFV 451
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Db        417 NGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFV 476

Qy        452 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 511
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Db        477 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 536

Qy        512 ENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAV 571
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Qy        632 HGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANL 691
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Qy        752 DVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREP 811
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Db        823 QQRLNIKEIYKILHALGKATPIYLDILG 850


RESULT 9
US-08-440-816A-7
; Sequence 7, Application US/08440816A
; Patent No. 5914237
;  GENERAL INFORMATION:
;    APPLICANT:  Godowski, Paul J.
;    APPLICANT:  Mark, Melanie R.
;    APPLICANT:  Sadick, Michael D.
;    APPLICANT:  Shelton, David L.
;    APPLICANT:  Wong, Wai Lee Tan
;    TITLE OF INVENTION:  KINASE RECEPTOR ACTIVATION ASSAY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/440,816A
;      FILING DATE:  15-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/286305
;      FILING DATE:  05-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/170558
;      FILING DATE:  20-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/157563
;      FILING DATE:  23-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lee, Wendy M.
;      REGISTRATION NUMBER:  00,000
;      REFERENCE/DOCKET NUMBER:  854C1P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1994
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  850 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-440-816A-7

  Query Match             93.9%;  Score 4222;  DB 2;  Length 850;
  Best Local Similarity   98.3%;  Pred. No. 0;
  Matches  794;  Conservative    0;  Mismatches    0;  Indels   14;  Gaps    1;

Qy         32 CPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENWRSL 91
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Db         57 CPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENWRSL 116

Qy         92 HTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQTLS 151
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Db        117 HTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQTLS 176

Qy        152 LRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCDLPE 211
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Qy        212 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 271
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Db        237 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 296

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Db        297 NVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPP 356

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Db        357 TLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTI 416

Qy        392 NGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFV 451
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Db        417 NGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFV 476

Qy        452 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 511
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Db        477 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 536

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RESULT 10
US-09-417-381A-7
; Sequence 7, Application US/09417381A
; Patent No. 6287784
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Sadick, Michael D.
; APPLICANT: Shelton, David L.
; APPLICANT: Wong, Wai Lee Tan
; TITLE OF INVENTION: KINASE RECEPTOR ACTIVATION ASSAY
; FILE REFERENCE: P0854C1P2C1
; CURRENT APPLICATION NUMBER: US/09/417,381A
; CURRENT FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 7
; LENGTH: 850
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-417-381A-7

Query Match 93.9%; Score 4222; DB 3; Length 850;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 794; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

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Qy        152 LRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCDLPE 211
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Db        177 LRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCDLPE 236

Qy        212 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 271
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Db        237 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 296

Qy        272 NVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPP 331
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 536

Qy        512 ENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAV 571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 ENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAV 596

Qy        572 KALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRA 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 KALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRA 656

Qy        632 HGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANL 691
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 HGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANL 716

Qy        692 LVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTES 751
              |||||||||||||||||||              ||||||||||||||||||||||||||||
Db        717 LVKIGDFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTES 762

Qy        752 DVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREP 811
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 DVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREP 822

Qy        812 QQRLNIKEIYKILHALGKATPIYLDILG 839
              ||||||||||||||||||||||||||||
Db        823 QQRLNIKEIYKILHALGKATPIYLDILG 850
```

RESULT 11
US-07-912-952-2
; Sequence 2, Application US/07912952
; Patent No. 5348856
; GENERAL INFORMATION:
; APPLICANT: Barbacid, Mariano
; APPLICANT: Lamballe, Fabienne
; TITLE OF INVENTION: TRKC PROTEIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burton Rodney
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/912,952
;       FILING DATE:  19920707
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Gaul, Timothy J.
;       REGISTRATION NUMBER:  33,111
;       REFERENCE/DOCKET NUMBER:  DC14a
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (609)252-4336
;       TELEFAX:  (609)252-4526
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  825 amino acids
;       TYPE:  AMINO ACID
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-07-912-952-2

  Query Match             92.8%;  Score 4172;  DB 1;  Length 825;
  Best Local Similarity   93.8%;  Pred. No. 0;
  Matches  789;  Conservative   12;  Mismatches   22;  Indels   18;  Gaps    3;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKSSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:|||||||||||||||||| |||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRGLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              |||||:||||:|||||||||||||||||||||||||||||||||||:||||||||||||
Db        181 KLNSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVVTCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              |:|||||||||||||||||||||||||||||||||||||||||| |||||||||:||
Db        301 VHYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKITHVEYYQEGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              |||||||||||||||||  : |||||||||||||||||||||||: | ||||||||||
Db        361 GCLLFNKPTHYNNGNYTLNRQEPLGTANQTINGHFLKEPFPESTDNFVSFYEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              |||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHIN--HGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538
              |||    |  |  :   ||    |||||||||||||||||||||||||||||||||||||
Db        481 LHHDQPWHHHTLITGRRAGHS--VIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538

Qy        539 VLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        539 VLKRELGEGAFGKVFLAECYNLSPTKVKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598

Qy        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAQGPDAMILVDGQPRQAKGELGLSQMLH 658

Qy        659 IASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGN 718
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 IASQICSGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR------- 711

Qy        719 DFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 778
              |||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db        712 -------VGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWDIFTYGKQPWFQLSNTE 764

Qy        779 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 838
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 824

Qy        839 G 839
              |
Db        825 G 825


RESULT 12
US-07-912-952-4
; Sequence 4, Application US/07912952
; Patent No. 5348856
;  GENERAL INFORMATION:
;    APPLICANT:  Barbacid, Mariano
;    APPLICANT:  Lamballe, Fabienne
;    TITLE OF INVENTION:  TRKC PROTEIN
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burton Rodney
;      STREET:  P.O. Box 4000
;      CITY:  Princeton
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  08543-4000
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/912,952
;      FILING DATE:  19920707
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gaul, Timothy J.
;      REGISTRATION NUMBER:  33,111
;      REFERENCE/DOCKET NUMBER:  DC14a
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (609)252-4336
;      TELEFAX:  (609)252-4526
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  728 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-912-952-4

  Query Match             81.7%;  Score 3673;  DB 1;  Length 728;
  Best Local Similarity   94.7%;  Pred. No. 2.8e-301;
  Matches  691;  Conservative   14;  Mismatches   21;  Indels    4;  Gaps    2;

Qy        112 NSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWM 171
              |||||:|||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db          1 NSGLRNIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWM 60

Qy        172 QLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITC 231
              |||||||||:|:|:||:||||:|||||||||||||||||||||||||||||||||||||
Db         61 QLWQEQGEARLDSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITC 120

Qy        232 NGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVG 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVG 180

Qy        292 MSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVE 351
              |||||||||||||||||| |||:|||||||||||||| |||||||:||||||||||::
Db        181 MSNASVALTVYYPPRVVSLVEPEVRLEHCIEFVVRGNPTPTLHWLYNGQPLRESKIIHMD 240
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Qy        352 YYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFD 411
              ||||||:|||||||||||||||||||||||| |||||||||||||||||||||| |
Db        241 YYQEGEVSEGCLLFNKPTHYNNGNYTLIAKNALGTANQTINGHFLKEPFPESTDFFDFES 300

Qy        412 EVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVI 471
              : |||||||||||||||||||||||||||||||:|||||||||||||||||||
Db        301 DASPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVI 360

Qy        472 SGEEDSASPLHHIN--HGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTY 529
              |||||||||||||    |  |    :       ||||||||||||||||||||||||||||
Db        361 SGEEDSASPLHHDQPWHHYTI--IVGCWAVHVVIGMTRIPVIENPQYFRQGHNCHKPDTY 418

Qy        530 VQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREA 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 VQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREA 478

Qy        590 ELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKG 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 ELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKG 538

Qy        650 ELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDY 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 ELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDY 598

Qy        710 YRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQ 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 YRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQ 658

Qy        770 PWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGK 829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 PWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGK 718

Qy        830 ATPIYLDILG 839
              ||||||||||
Db        719 ATPIYLDILG 728
```

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RESULT 13
US-08-359-705B-8
; Sequence 8, Application US/08359705B
; Patent No. 5844092
;  GENERAL INFORMATION:
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shelton, David L.
;    APPLICANT:  Urfer, Roman
;    TITLE OF INVENTION:  Human trk Receptors and Neurotrophic Factor Inhibitors
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/359,705B
;      FILING DATE:  20-Dec-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/286846
;      FILING DATE:  08/10/94
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/215139
;      FILING DATE:  03/18/94
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, PhD., Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  P0873P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-8674
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  612 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-359-705B-8

  Query Match             63.1%;  Score 2836;  DB 2;  Length 612;
  Best Local Similarity   99.8%;  Pred. No. 9.7e-231;
  Matches  529;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYV 530
              |||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTWV 530
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```
RESULT 14
US-08-286-846A-8
; Sequence 8, Application US/08286846A
; Patent No. 5877016
;  GENERAL INFORMATION:
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shelton, David L.
;    APPLICANT:  Urfer, Roman
;    TITLE OF INVENTION:  Human trk Receptors and Neurotrophic Factor Inhibitors
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/286,846A
;      FILING DATE:  05-Aug-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, PhD., Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  P0873P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8674
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  612 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-286-846A-8

  Query Match             63.1%;  Score 2836;  DB 2;  Length 612;
  Best Local Similarity   99.8%;  Pred. No. 9.7e-231;
  Matches  529;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYV 530
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RESULT 15
US-08-457-880A-8
; Sequence 8, Application US/08457880A
; Patent No. 5910574
;  GENERAL INFORMATION:
;    APPLICANT:  Leonard G. Presta
;    APPLICANT:  David L. Shelton
;    APPLICANT:  Roman Urfer
;    TITLE OF INVENTION:  HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR
;    TITLE OF INVENTION:  INHIBITORS
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,880A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,622
;      FILING DATE:  19-May-1995
;      APPLICATION NUMBER:  08/286846
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Torchia, PhD., Timothy E.
;      REGISTRATION NUMBER:  36,700
;      REFERENCE/DOCKET NUMBER:  P0873P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-8674
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  612 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-457-880A-8

  Query Match             63.1%;  Score 2836;  DB 2;  Length 612;
  Best Local Similarity   99.8%;  Pred. No. 9.7e-231;
  Matches  529;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
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Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
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Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
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Search completed: July 12, 2004, 13:40:05
Job time : 26 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:38:56 ; Search time 56 Seconds
(without alignments)
4673.204 Million cell updates/sec

Title: US-09-966-147-6
Perfect score: 4497
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4497	100.0	839	9	US-09-966-147-6	Sequence 6, Appli
2	4497	100.0	839	12	US-10-698-597-6	Sequence 6, Appli
3	4497	100.0	839	12	US-09-960-498-16	Sequence 16, Appl
4	4497	100.0	839	14	US-10-374-469-6	Sequence 6, Appli
5	4492	99.9	839	16	US-10-645-546-14	Sequence 14, Appl
6	4358.5	96.9	864	12	US-09-960-498-15	Sequence 15, Appl
7	4222	93.9	850	9	US-09-924-859A-7	Sequence 7, Appli
8	2836	63.1	612	9	US-09-966-147-8	Sequence 8, Appli
9	2836	63.1	612	12	US-10-698-597-8	Sequence 8, Appli
10	2836	63.1	612	14	US-10-374-469-8	Sequence 8, Appli
11	2610	58.0	576	16	US-10-287-226-284	Sequence 284, App
12	2287.5	50.9	821	12	US-09-960-498-13	Sequence 13, Appl
13	2287.5	50.9	821	14	US-10-205-219-11	Sequence 11, Appl
14	2287.5	50.9	821	16	US-10-645-546-10	Sequence 10, Appl
15	2277	50.6	822	9	US-09-966-147-2	Sequence 2, Appli
16	2277	50.6	822	12	US-10-698-597-2	Sequence 2, Appli
17	2277	50.6	822	12	US-09-960-498-14	Sequence 14, Appl
18	2277	50.6	822	14	US-10-374-469-2	Sequence 2, Appli
19	2277	50.6	822	15	US-10-366-288-24	Sequence 24, Appl
20	2277	50.6	822	15	US-10-295-027-394	Sequence 394, App
21	2277	50.6	822	15	US-10-295-027-1272	Sequence 1272, Ap
22	2277	50.6	822	16	US-10-645-546-2	Sequence 2, Appli
23	2259.5	50.2	847	9	US-09-924-859A-5	Sequence 5, Appli
24	2259	50.2	838	15	US-10-295-027-396	Sequence 396, App
25	2062.5	45.9	387	12	US-09-960-498-2	Sequence 2, Appli
26	1989.5	44.2	393	12	US-09-960-498-3	Sequence 3, Appli
27	1961	43.6	796	12	US-09-960-498-12	Sequence 12, Appl
28	1960	43.6	790	9	US-09-966-147-9	Sequence 9, Appli
29	1960	43.6	790	12	US-10-698-597-9	Sequence 9, Appli
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32	1950	43.4	790	16	US-10-276-272A-18	Sequence 18, Appl
33	1913	42.5	799	12	US-09-960-498-11	Sequence 11, Appl
34	1400.5	31.1	729	16	US-10-276-272A-15	Sequence 15, Appl
35	1400.5	31.1	930	16	US-10-276-272A-13	Sequence 13, Appl
36	1399.5	31.1	731	16	US-10-276-272A-16	Sequence 16, Appl
37	1396.5	31.1	732	16	US-10-276-272A-14	Sequence 14, Appl
38	1299.5	28.9	641	14	US-10-242-943-4	Sequence 4, Appli
39	979.5	21.8	537	16	US-10-645-546-6	Sequence 6, Appli
40	961.5	21.4	553	16	US-10-645-546-8	Sequence 8, Appli
41	801	17.8	868	13	US-10-016-283-1	Sequence 1, Appli
42	795.5	17.7	869	13	US-10-016-283-33	Sequence 33, Appl
43	792.5	17.6	869	9	US-09-817-487A-2	Sequence 2, Appli
44	773	17.2	476	16	US-10-645-546-12	Sequence 12, Appl
45	763.5	17.0	477	9	US-09-966-147-4	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
US-09-966-147-6
; Sequence 6, Application US/09966147
; Patent No. US20020146416A1
;  GENERAL INFORMATION:
;       APPLICANT: Presta, Leonard G.
;                  Shelton, David L.
;                  Urfer, Roman
;       TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS
;       NUMBER OF SEQUENCES: 41
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
;            STREET: 620 Newport Center Drive, 16th Floor
;            CITY: Newport Beach
;            STATE: California
;            COUNTRY: USA
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,147
;            FILING DATE: 27-Sep-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/446172
;            FILING DATE: 19-MAY-1995
;            APPLICATION NUMBER: 08/286846
;            FILING DATE: 05-AUG-1994
;            APPLICATION NUMBER: 08/215139
;            FILING DATE: 18-MAR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Dreger, Ginger
;            REGISTRATION NUMBER: 33,055
;            REFERENCE/DOCKET NUMBER: GENENT.33CPC4C
;       TELECOMMUNICATION INFORMATION:
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;             TELEPHONE: (415) 954-4114
;             TELEFAX: (415) 954-4111
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 839 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-966-147-6

  Query Match           100.0%;  Score 4497;  DB 9;  Length 839;
  Best Local Similarity  100.0%;  Pred. No. 0;
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Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
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Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
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Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
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Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

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RESULT 2
US-10-698-597-6
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; Sequence 6, Application US/10698597
; Publication No. US20040058416A1
;  GENERAL INFORMATION:
;       APPLICANT: Presta, Leonard G.
;                  Shelton, David L.
;                  Urfer, Roman
;       TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor
;                           Inhibitors
;       NUMBER OF SEQUENCES: 41
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear
;            STREET: 620 Newport Center Drive 16th Floor
;            CITY: Newport Beach
;            STATE: California
;            COUNTRY: USA
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
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;            FILING DATE: 31-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/724,524
;            FILING DATE: 27-No. US20040058416A1-2000
;            APPLICATION NUMBER: 09/156,923
;            FILING DATE: 18-SEP-1998
;            APPLICATION NUMBER: 08/359,705
;            FILING DATE: 20-DEC-1994
;            APPLICATION NUMBER: 08/286846
;            FILING DATE: 10-AUG-1994
;            APPLICATION NUMBER: 08/215139
;            FILING DATE: 18-MAR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Dreger, Ginger
;            REGISTRATION NUMBER: 33,055
;            REFERENCE/DOCKET NUMBER: GENENT.33CP2C2
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 949/760-0404
;            TELEFAX: 949/760-9502
;   INFORMATION FOR SEQ ID NO: 6:
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;            TOPOLOGY: Linear
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US-10-698-597-6

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Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
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Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839


RESULT 3
US-09-960-498-16
; Sequence 16, Application US/09960498
; Publication No. US20020039966A1
; GENERAL INFORMATION:
;  APPLICANT: Bates, Alan T.
;  TITLE OF INVENTION: MODULATORS OF TRK PROTEIN ACTIVITY, COMPOSITIONS AND METHODS OF U
;  FILE REFERENCE: A-69548/RMS/DHR
;  CURRENT APPLICATION NUMBER: US/09/960,498
;  CURRENT FILING DATE:  2001-07-05
;  PRIOR APPLICATION NUMBER: US 60/215,778
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 839
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-960-498-16

  Query Match           100.0%;  Score 4497;  DB 12;  Length 839;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839


RESULT 4
US-10-374-469-6
; Sequence 6, Application US/10374469
; Publication No. US20030157099A1
;  GENERAL INFORMATION:
;       APPLICANT: Presta, Leonard G.
;                  Shelton, David L.
;                  Urfer, Roman
;       TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS
;       NUMBER OF SEQUENCES: 41
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
;            STREET: 620 Newport Center Drive, 16th Floor
;            CITY: Newport Beach
;            STATE: California
;            COUNTRY: USA
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/374,469
;            FILING DATE: 24-Feb-2003
;            CLASSIFICATION: <Unknown>
```

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;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,147
;            FILING DATE: 27-Sep-2000
;            APPLICATION NUMBER: 08/446172
;            FILING DATE: 19-MAY-1995
;            APPLICATION NUMBER: 08/286846
;            FILING DATE: 05-AUG-1994
;            APPLICATION NUMBER: 08/215139
;            FILING DATE: 18-MAR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Dreger, Ginger
;            REGISTRATION NUMBER: 33,055
;            REFERENCE/DOCKET NUMBER: GENENT.33CPC4C
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 954-4114
;            TELEFAX: (415) 954-4111
;   INFORMATION FOR SEQ ID NO: 6:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 839 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-374-469-6

  Query Match           100.0%;  Score 4497;  DB 14;  Length 839;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839


RESULT 5
US-10-645-546-14
; Sequence 14, Application US/10645546
; Publication No. US20040110711A1
; GENERAL INFORMATION:
;  APPLICANT: Krueger, Bruce K.
;  APPLICANT:  Kingsbury, Tami J.
;  APPLICANT:  Bambrick, Linda L.
;  APPLICANT:  Dorsey, Susan G.
;  TITLE OF INVENTION: Novel Treatment of Neurodegenerative Diseases by Altering
;  TITLE OF INVENTION:  Levels of TrkB Isoforms and/or TrkC Isoforms
;  FILE REFERENCE: 028754-042
;  CURRENT APPLICATION NUMBER: US/10/645,546
;  CURRENT FILING DATE:  2003-08-22
;  PRIOR APPLICATION NUMBER: US 60/270,553
;  PRIOR FILING DATE: 2001-02-22
;  PRIOR APPLICATION NUMBER: PCT/US02/05151
;  PRIOR FILING DATE: 2002-02-22
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 839
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NCBI/XM_038336
;   DATABASE ENTRY DATE: 2002-02-07
US-10-645-546-14

  Query Match           99.9%;  Score 4492;  DB 16;  Length 839;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  838;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
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Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
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RESULT 6
US-09-960-498-15
; Sequence 15, Application US/09960498
; Publication No. US20020039966A1
; GENERAL INFORMATION:
; APPLICANT: Bates, Alan T.
; TITLE OF INVENTION: MODULATORS OF TRK PROTEIN ACTIVITY, COMPOSITIONS AND METHODS OF U
; FILE REFERENCE: A-69548/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/960,498
; CURRENT FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: US 60/215,778
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 864
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-960-498-15

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  Query Match             96.9%;  Score 4358.5;  DB 12;  Length 864;
  Best Local Similarity   94.3%;  Pred. No. 0;
  Matches  815;  Conservative   14;  Mismatches   10;  Indels   25;  Gaps    1;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:||||||||||||||||||| |||||||||||||||||||||||||||:|||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRGLHTLNAVDMELYTGLQKLTIKNSGLRNIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              :|:||:||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RLDSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              |||||||||| ||| :|||||||||||||| ||||||:||||||||||||::||||||:||
Db        301 VYYPPRVVSLVEPEVRLEHCIEFVVRGNPTPTLHWLYNGQPLRESKIIHMDYYQEGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              |||||||||||||||||||||| |||||||||||||||||||||| |    : |||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNALGTANQTINGHFLKEPFPESTDFFDFESDASPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR--------- 711
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYREGPYQKGPF 720

Qy        712 ---------------LFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWS 755
                             ||||||||||||||||||||||||||||||||||||||||||||
Db        721 SVSWQQRLAASAASTLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWS 780

Qy        756 FGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRL 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 FGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRL 840

Qy        816 NIKEIYKILHALGKATPIYLDILG 839
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Db        841 NIKEIYKILHALGKATPIYLDILG 864
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RESULT 7
US-09-924-859A-7
; Sequence 7, Application US/09924859A
; Patent No. US20020137113A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Sadick, Michael D.
; APPLICANT: Shelton, David L.
; APPLICANT: Wong, Wai Lee Tan
; TITLE OF INVENTION: KINASE RECEPTOR ACTIVATION ASSAY
; FILE REFERENCE: P0854C1P2C1
; CURRENT APPLICATION NUMBER: US/09/924,859A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US/09/417,381
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 7
;   LENGTH: 850
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-924-859A-7

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  Query Match             93.9%;  Score 4222;  DB 9;  Length 850;
  Best Local Similarity   98.3%;  Pred. No. 2.3e-309;
  Matches  794;  Conservative    0;  Mismatches    0;  Indels   14;  Gaps    1;

Qy         32 CPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENWRSL 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         57 CPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENWRSL 116

Qy         92 HTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQTLS 151
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Db        117 HTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQTLS 176

Qy        152 LRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCDLPE 211
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 LRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCDLPE 236

Qy        212 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 271
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 ISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLV 296

Qy        272 NVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPP 331
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 NVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPP 356

Qy        332 TLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTI 391
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 TLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTI 416

Qy        392 NGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFV 451
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 NGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFV 476

Qy        452 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 511
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 MINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVI 536

Qy        512 ENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAV 571
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 ENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAV 596

Qy        572 KALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRA 631
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 KALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRA 656

Qy        632 HGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANL 691
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 HGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANL 716

Qy        692 LVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTES 751
                ||||||||||||||||||||              ||||||||||||||||||||||||
Db        717 LVKIGDFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTES 762

Qy        752 DVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREP 811
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 DVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREP 822

Qy        812 QQRLNIKEIYKILHALGKATPIYLDILG 839
                |||||||||||||||||||||||||||
Db        823 QQRLNIKEIYKILHALGKATPIYLDILG 850


RESULT 8
US-09-966-147-8
; Sequence 8, Application US/09966147
; Patent No. US20020146416A1
;   GENERAL INFORMATION:
;       APPLICANT: Presta, Leonard G.
;                  Shelton, David L.
;                  Urfer, Roman
;       TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS
;       NUMBER OF SEQUENCES: 41
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
;            STREET: 620 Newport Center Drive, 16th Floor
;            CITY: Newport Beach
;            STATE: California
;            COUNTRY: USA
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,147
;            FILING DATE: 27-Sep-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/446172
;            FILING DATE: 19-MAY-1995
;            APPLICATION NUMBER: 08/286846
;            FILING DATE: 05-AUG-1994
;            APPLICATION NUMBER: 08/215139
;            FILING DATE: 18-MAR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Dreger, Ginger
;            REGISTRATION NUMBER: 33,055
;            REFERENCE/DOCKET NUMBER: GENENT.33CPC4C
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 954-4114
;            TELEFAX: (415) 954-4111
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 612 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-966-147-8

  Query Match            63.1%;  Score 2836;  DB 9;  Length 612;
  Best Local Similarity  99.8%;  Pred. No. 4.7e-205;
  Matches  529;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYV 530
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Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTWV 530


RESULT 9
US-10-698-597-8
; Sequence 8, Application US/10698597
; Publication No. US20040058416A1
;   GENERAL INFORMATION:
```

```
;       APPLICANT: Presta, Leonard G.
;                  Shelton, David L.
;                  Urfer, Roman
;       TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor
;                           Inhibitors
;       NUMBER OF SEQUENCES: 41
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear
;            STREET: 620 Newport Center Drive 16th Floor
;            CITY: Newport Beach
;            STATE: California
;            COUNTRY: USA
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/698,597
;            FILING DATE: 31-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/724,524
;            FILING DATE: 27-No. US20040058416A1-2000
;            APPLICATION NUMBER: 09/156,923
;            FILING DATE: 18-SEP-1998
;            APPLICATION NUMBER: 08/359,705
;            FILING DATE: 20-DEC-1994
;            APPLICATION NUMBER: 08/286846
;            FILING DATE: 10-AUG-1994
;            APPLICATION NUMBER: 08/215139
;            FILING DATE: 18-MAR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Dreger, Ginger
;            REGISTRATION NUMBER: 33,055
;            REFERENCE/DOCKET NUMBER: GENENT.33CP2C2
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 949/760-0404
;            TELEFAX: 949/760-9502
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 612 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-698-597-8

  Query Match            63.1%;  Score 2836;  DB 12;  Length 612;
  Best Local Similarity  99.8%;  Pred. No. 4.7e-205;
  Matches  529;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYV 530
              |||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTWV 530


RESULT 10
US-10-374-469-8
; Sequence 8, Application US/10374469
; Publication No. US20030157099A1
;   GENERAL INFORMATION:
;       APPLICANT: Presta, Leonard G.
;                  Shelton, David L.
;                  Urfer, Roman
;       TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS
;       NUMBER OF SEQUENCES: 41
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
;            STREET: 620 Newport Center Drive, 16th Floor
;            CITY: Newport Beach
;            STATE: California
;            COUNTRY: USA
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/374,469
;            FILING DATE: 24-Feb-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/966,147
;            FILING DATE: 27-Sep-2000
;            APPLICATION NUMBER: 08/446172
;            FILING DATE: 19-MAY-1995
;            APPLICATION NUMBER: 08/286846
;            FILING DATE: 05-AUG-1994
;            APPLICATION NUMBER: 08/215139
;            FILING DATE: 18-MAR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Dreger, Ginger
;            REGISTRATION NUMBER: 33,055
;            REFERENCE/DOCKET NUMBER: GENENT.33CPC4C
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 954-4114
;            TELEFAX: (415) 954-4111
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 612 amino acids
;            TYPE: Amino Acid
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-374-469-8

  Query Match            63.1%;  Score 2836;  DB 14;  Length 612;
  Best Local Similarity  99.8%;  Pred. No. 4.7e-205;
  Matches  529;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
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Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYV 530
              ||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTWV 530
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RESULT 11
US-10-287-226-284
; Sequence 284, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
;  APPLICANT: Agee, Michele L.,
;  APPLICANT:  Alsobrook, John P.,
;  APPLICANT:  Berghs, Constance,
;  APPLICANT:  Boldog, Ference,
;  APPLICANT:  Burgess, Catherine E.,
;  APPLICANT:  Chant, John S.,
;  APPLICANT:  Chaudhuri, Amitabha,
;  APPLICANT:  DiPippo, Vincent A.,
;  APPLICANT:  Edinger, Shlomit R.,
;  APPLICANT:  Eisen, Andrew,
;  APPLICANT:  Ellerman, Karen,
;  APPLICANT:  Gangolli, Esha A.,
;  APPLICANT:  Gorman, Linda,
;  APPLICANT:  Gerlach, Valerie,
;  APPLICANT:  Ji, Weizhen,
;  APPLICANT:  Kekuda, Ramesh,
;  APPLICANT:  Khramtsov, Nikolai,
;  APPLICANT:  Li, Li,
;  APPLICANT:  Malyankar, Uriel M.,
;  APPLICANT:  MacDougall, John R.,
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Miller, Charles E.,
;  APPLICANT:  Millet, Isabelle,
;  APPLICANT:  Ooi, Chean Eng,
;  APPLICANT:  Ort, Tatiana,
;  APPLICANT:  Padigaru, Muralidhara,
;  APPLICANT:  Patturajan, Meera,
;  APPLICANT:  Rastelli, Luca,
;  APPLICANT:  Rieger, Daniel K.,
;  APPLICANT:  Rothenberg, Mark E.,
;  APPLICANT:  Shenoy, Suresh G.,
;  APPLICANT:  Spaderna, Steven K.,
;  APPLICANT:  Spytek, Kimberley A.,
;  APPLICANT:  Taupier, Jr., Raymond J.,
;  APPLICANT:  Vernet, Corine A.M.,
;  APPLICANT:  Zerhusen, Bryan D.,
;  APPLICANT:  Zhong, Mei
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-480C
;  CURRENT APPLICATION NUMBER: US/10/287,226
;  CURRENT FILING DATE:  2002-11-04
;  PRIOR APPLICATION NUMBER: 60/334,421
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,392
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/360,148
;  PRIOR FILING DATE: 2002-02-27
;  PRIOR APPLICATION NUMBER: 60/364,000
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/404,821
;  PRIOR FILING DATE: 2002-08-20
;  PRIOR APPLICATION NUMBER: 60/334,526
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: 60/354,409
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: 60/364,227
;  PRIOR FILING DATE: 2002-03-13
;  PRIOR APPLICATION NUMBER: 60/334,027
;  PRIOR FILING DATE: 2001-11-28
;  PRIOR APPLICATION NUMBER: 60/331,641
;  PRIOR FILING DATE: 2001-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 673
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 284
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-226-284

  Query Match            58.0%;  Score 2610;  DB 16;  Length 576;
  Best Local Similarity  97.6%;  Pred. No. 4.7e-188;
  Matches  490;  Conservative    3;  Mismatches    1;  Indels    8;  Gaps    1;

Qy         29 VLACPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENW 88
              ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db          1 VLACPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNASINITDISRNITSIHIENW 60

Qy         89 RSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQ 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQ 120

Qy        149 TLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCD 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFRMNISQCD 180

Qy        209 LPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINL 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINL 240

Qy        269 TLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGN 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRGN 300

Qy        329 PPPTLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTAN 388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 PPPTLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTAN 360

Qy        389 QTINGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVV 448
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        361 QTINGHFLKEPFP--------VDEVSPTPPITVTHKPEEDTFGVSIAVGLAAFACVLLVV 412

Qy        449 LFVMINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRI 508
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 VFVMINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRI 472

Qy        509 PVIENPQYFRQGHNCHKPDTYV 530
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                    ||||||||||||||||||||:|
Db        473 PVIENPQYFRQGHNCHKPDTWV 494


RESULT 12
US-09-960-498-13
; Sequence 13, Application US/09960498
; Publication No. US20020039966A1
; GENERAL INFORMATION:
;  APPLICANT: Bates, Alan T.
;  TITLE OF INVENTION: MODULATORS OF TRK PROTEIN ACTIVITY, COMPOSITIONS AND METHODS OF U
;  FILE REFERENCE: A-69548/RMS/DHR
;  CURRENT APPLICATION NUMBER: US/09/960,498
;  CURRENT FILING DATE:  2001-07-05
;  PRIOR APPLICATION NUMBER: US 60/215,778
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
;   LENGTH: 821
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-960-498-13

  Query Match             50.9%;  Score 2287.5;  DB 12;  Length 821;
  Best Local Similarity   54.0%;  Pred. No. 1.6e-163;
  Matches  468;  Conservative  106;  Mismatches  204;  Indels   89;  Gaps   16;

Qy          7 PAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDSGNS 65
              ||     | : ||     | :  : |||| :| || | | |  |  | : || ||
Db         10 PAMARLWGLCLL---VLGFWRASLACPMSCKCSTTRIWCTEPSPGIVAFPRLEP------ 60

Qy         66 NGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAK 125
                 |  |   ||| | | | : |  :|  |:| | ||: ||| :|||: :  :|| |
Db         61 ------NSID-PENITEILIANQKRLEIINEDDVEAYVGLKNLTIVDSGLKFVAYKAFLK 113

Qy        126 NPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQ 185
              | :||:|| : |:||:|| : |: | | :| |  | | ||||| |::  ||  ::  ::|
Db        114 NGNLRHINFTRNKLTSLSRRHFRHLDLSDLILTGNPFTCSCDIMWLKTLQET-KSSPDTQ 172

Qy        186 NLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIV 245
              :|||:|      ||  : |  | ||   ::  |||| || :  |:|:  | ||| : | |
Db        173 DLYCLNESSKNTPLANLQIPNCGLPSARLAAPNLTVEEGKSVTISCSVGGDPLPTLYWDV 232

Qy        246 TGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPP 305
                | |      ::| |:    :| : |::|:|:|  ::|:|||:||    || |||:: |
Db        233 GNLVS-----KHMNETSHTQGSLRITNISSDDSGKQISCVAENLVGEDQDSVNLTVHFAP 287

Qy        306 RVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKII--------HVEYYQEGE 357
              :  || |       || | ||||| | | | :||  | ||| |         | ||:
Db        288 TITFLESPTSDHHWCIPFTVRGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYH---- 343

Qy        358 ISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEP---------FPESTDNFI 408
                 |||  : ||| |||:|||:|||  |   : |: ||:  |           :||     :
Db        344 ---GCLQLDNPTHMNNGDYTLMAKNEYGKDERQISAHFMGRPGVDYETNPNYPE-----V 395

Qy        409 LFDE-VSPTPPITVTHKPEE---------------DTFGVSIAVGLAAFACVLLVVLFVM 452
              |:::  :||      |:|  |               : | :   :  | |:|:::| :
Db        396 LYEDWTTPTDIGDTTNKSNEIPSTDVADQTNREHLSVYAVVVIASVVGF-CLLVMLLL- 453

Qy        453 INKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIE 512
                |  | |||||||| :||| ::|||||||||::|  |||| : ||| |:||||:|||||
Db        454 --KLARHSKFGMKGPASVISNDDDSASPLHHISNGSNTPSSSEGGPDAVIIGMTKIPVIE 511

Qy        513 NPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVK 572
              |||||   ::  ||||:|||||| :|||||||||||||||||||||| | :||:|||||
Db        512 NPQYFGITNSQLKPDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLCPEQDKILVAVK 571

Qy        573 ALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAH 632
              |||  :  ||||| |||||||||||||||||||| :|||||||||||||||||||||||
Db        572 TLKDASDNARKDFHREAELLTNLQHEHIVKFYGVCVEGDPLIMVFEYMKHGDLNKFLRAH 631

Qy        633 GPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLL 692
              ||||::: :| |     ||  ||||||| |||:|||||||||||||||||||||||| |||
Db        632 GPDAVLMAEGNP---PTELTQSQMLHIAQQIAAGMVYLASQHFVHRDLATRNCLVGENLL 688

Qy        693 VKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESD 752
              ||||||||||||||||||                  |||||||||||||||||||||||||
Db        689 VKIGDFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTESD 734

Qy        753 VWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQ 812
              ||| ||:|||||||||||:|||| ||||||||||||:||| ||:|||::|||||||||
Db        735 VWSLGVVLWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPQEVYELMLGCWQREPH 794

Qy        813 QRLNIKEIYKILHALGKATPIYLDILG 839
              | ||| |: :|  | ||:|:||||||
Db        795 TRKNIKNIHTLLQNLAKASPVYLDILG 821


RESULT 13
US-10-205-219-11
; Sequence 11, Application US/10205219
; Publication No. US20030138803A1
; GENERAL INFORMATION:
;  APPLICANT: Warner-Lambert Company
;  APPLICANT:  Lee, Kevin
;  APPLICANT:  Dixon, Alistair
;  APPLICANT:  Brooksbank, Robert
;  APPLICANT:  Pinnock, Robert
;  TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
;  FILE REFERENCE: WL-A-018200
;  CURRENT APPLICATION NUMBER: US/10/205,219
;  CURRENT FILING DATE:  2002-07-24
;  PRIOR APPLICATION NUMBER: GB 0118354.0
;  PRIOR FILING DATE: 2001-07-27
;  NUMBER OF SEQ ID NOS: 197
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 821
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: Neural receptor protein-tyrosine kinase
US-10-205-219-11

  Query Match             50.9%;  Score 2287.5;  DB 14;  Length 821;
  Best Local Similarity   54.0%;  Pred. No. 1.6e-163;
  Matches  468;  Conservative  106;  Mismatches  204;  Indels   89;  Gaps   16;

Qy          7 PAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDSGNS 65
              ||     | : ||     | :  : |||| :| || | | |  |  | : || ||
Db         10 PAMARLWGLCLL---VLGFWRASLACPMSCKCSTTRIWCTEPSPGIVAFPRLEP------ 60

Qy         66 NGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAK 125
                 |  |   ||| | | | : |  :|  |:| | ||: ||| :|||: :  :|| |
Db         61 ------NSID-PENITEILIANQKRLEIINEDDVEAYVGLKNLTIVDSGLKFVAYKAFLK 113

Qy        126 NPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQ 185
              | :||:|| : |:||:|| : |: | | :| |  | | ||||| |::  ||  ::  ::|
Db        114 NGNLRHINFTRNKLTSLSRRHFRHLDLSDLILTGNPFTCSCDIMWLKTLQET-KSSPDTQ 172

Qy        186 NLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIV 245
              :|||:|      ||  : |  | ||   ::  |||| || :  |:|:  | ||| : | |
Db        173 DLYCLNESSKNTPLANLQIPNCGLPSARLAAPNLTVEEGKSVTISCSVGGDPLPTLYWDV 232

Qy        246 TGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPP 305
                | |      ::| |:    :| : |::|:|:|  ::|:|||:||    || |||:: |
Db        233 GNLVS-----KHMNETSHTQGSLRITNISSDDSGKQISCVAENLVGEDQDSVNLTVHFAP 287

Qy        306 RVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKII--------HVEYYQEGE 357
              :  || |       || | ||||| | | | :||  | ||| |         | ||:
Db        288 TITFLESPTSDHHWCIPFTVRGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYH---- 343

Qy        358 ISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEP---------FPESTDNFI 408
                 |||  : ||| |||:|||:|||  |   : |: ||:  |           :||     :
Db        344 ---GCLQLDNPTHMNNGDYTLMAKNEYGKDERQISAHFMGRPGVDYETNPNYPE-----V 395
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Qy        409 LFDE-VSPTPPITVTHKPEE--------------DTFGVSIAVGLAAFACVLLVVLFVM 452
Db        396 LYEDWTTPTDIGDTTNKSNEIPSTDVADQTNREHLSVYAVVVIASVVGF-CLLVMLLLL- 453

Qy        453 INKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIE 512
Db        454 --KLARHSKFGMKGPASVISNDDDSASPLHHISNGSNTPSSSEGGPDAVIIGMTKIPVIE 511

Qy        513 NPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVK 572
Db        512 NPQYFGITNSQLKPDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLCPEQDKILVAVK 571

Qy        573 ALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAH 632
Db        572 TLKDASDNARKDFHREAELLTNLQHEHIVKFYGVCVEGDPLIMVFEYMKHGDLNKFLRAH 631

Qy        633 GPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLL 692
Db        632 GPDAVLMAEGNP---PTELTQSQMLHIAQQIAAGMVYLASQHFVHRDLATRNCLVGENLL 688

Qy        693 VKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESD 752
Db        689 VKIGDFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTESD 734

Qy        753 VWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQ 812
Db        735 VWSLGVVLWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPQEVYELMLGCWQREPH 794

Qy        813 QRLNIKEIYKILHALGKATPIYLDILG 839
Db        795 TRKNIKNIHTLLQNLAKASPVYLDILG 821
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RESULT 14
US-10-645-546-10
; Sequence 10, Application US/10645546
; Publication No. US20040110711A1
; GENERAL INFORMATION:
; APPLICANT: Krueger, Bruce K.
; APPLICANT: Kingsbury, Tami J.
; APPLICANT: Bambrick, Linda L.
; APPLICANT: Dorsey, Susan G.
; TITLE OF INVENTION: Novel Treatment of Neurodegenerative Diseases by Altering
; TITLE OF INVENTION: Levels of TrkB Isoforms and/or TrkC Isoforms
; FILE REFERENCE: 028754-042
; CURRENT APPLICATION NUMBER: US/10/645,546
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: US 60/270,553
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US02/05151
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/X17647
; DATABASE ENTRY DATE: 1995-03-22
; RELEVANT RESIDUES: (1)..(821)
US-10-645-546-10

Query Match 50.9%; Score 2287.5; DB 16; Length 821;
Best Local Similarity 54.0%; Pred. No. 1.6e-163;
Matches 466; Conservative 110; Mismatches 206; Indels 81; Gaps 15;

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Qy          7 PAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDSGNS 65
Db         10 PAMARLWGLCLL---VLGFWRASLACPTSCKCSSARIWCTEPSPGIVAFPRLEP------ 60

Qy         66 NGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAK 125
Db         61 ------NSVD-PENITEILIANQKRLEIINEDDVEAYVGLRNLTIVDSGLKFVAYKAFLK 113

Qy        126 NPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQ 185
Db        114 NSNLRHINFTRNKLTSLSRRHFRHLDLSDLILTGNPFTCSCDIMWLKTLQET-KSSPDTQ 172

Qy        186 NLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIV 245
Db        173 DLYCLNESSKNMPLANLQIPNCGLPSARLAAPNLTVEEGKSVTLSCSVGGDPLPTLYWDV 232

Qy        246 TGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPP 305
Db        233 GNLVS-----KHMNETSHTQGSLRITNISSDDSGKQISCVAENLVGEDQDSVNLTVHFAP 287

Qy        306 RVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKII--------HVEYYQEGE 357
Db        288 TITFLESPTSDHHWCIPFTVRGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYH---- 343

Qy        358 ISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEP---------FPESTDNFI 408
Db        344 ---GCLQLDNPTHMNNGDYTLMAKNEYGKDERQISAHFMGRPGVDYETNPNYPE-----V 395

Qy        409 LFDE-VSPTPPITVTHK----PEEDTFGVSIAVGLAAFACVLL-------VVLFVMINKY 456
Db        396 LYEDWTTPTDIGDTTNKSNEIPSTDVADQSNREHLSVYAVVVIASVVGFCLLVMLLLLKL 455

Qy        457 GRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQY 516
Db        456 ARHSKFGMKGPASVISNDDDSASPLHHISNGSNTPSSSEGGPDAVIIGMTKIPVIENPQY 515

Qy        517 FRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKD 576
Db        516 FGITNSQLKPDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLCPEQDKILVAVKTLKD 575

Qy        577 PTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDA 636
Db        576 ASDNARKDFHREAELLTNLQHEHIVKFYGVCVEGDPLIMVFEYMKHGDLNKFLRAHGPDA 635

Qy        637 MILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIG 696
Db        636 VLMAEGNP---PTELTQSQMLHIAQQIAAGMVYLASQHFVHRDLATRNCLVGENLLVKIG 692

Qy        697 DFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSF 756
Db        693 DFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTESDVWSL 738

Qy        757 GVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLN 816
Db        739 GVVLWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPQEVYELMLGCWQREPHTRKN 798

Qy        817 IKEIYKILHALGKATPIYLDILG 839
Db        799 IKSIHTLLQNLAKASPVYLDILG 821
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RESULT 15
US-09-966-147-2
; Sequence 2, Application US/09966147
; Patent No. US20020146416A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Shelton, David L.
; Urfer, Roman
; TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: USA
; ZIP: 92660

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/966,147
; FILING DATE: 27-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446172
; FILING DATE: 19-MAY-1995
; APPLICATION NUMBER: 08/286846
; FILING DATE: 05-AUG-1994
; APPLICATION NUMBER: 08/215139
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: GENENT.33CPC4C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 954-4114
; TELEFAX: (415) 954-4111
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-966-147-2

Query Match 50.6%; Score 2277; DB 9; Length 822;
Best Local Similarity 53.7%; Pred. No. 9.8e-163;
Matches 467; Conservative 110; Mismatches 199; Indels 94; Gaps 18;

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Qy          7 PAKCSFWRIFLLGSVWLDYVG---SVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDS 62
              ||    |     |  ||  ||   :  ||| :| || : | |  |  | : || ||
Db         10 PAMARLW-----GFCWL-VVGFWRAAFACPTSCKCSASRIWCSDPSPGIVAFPRLEP--- 60

Qy         63 GNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRA 122
                  |  |   ||| | | | :  |  :|  |:| | ||: ||| :|||: :  :|
Db         61 ---------NSVD-PENITEIFIANQKRLEIINEDDVEAYVGLRNLTIVDSGLKFVAHKA 110

Qy        123 FAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKL 182
              | || :|::|| : |:||:|| : |:  | | || |  | | ||||| |::  ||  ::
Db        111 FLKNSNLQHINFTRNKLTSLSRKHFRHLDLSELILVGNPFTCSCDIMWIKTLQE-AKSSP 169

Qy        183 NSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVD 242
              ::|:|||:|     :||  : |  | ||  :::  |||| || :  ::|: :| |:|::
Db        170 DTQDLYCLNESSKNIPLANLQIPNCGLPSANLAAPNLTVEEGKSITLSCSVAGDPVPNMY 229

Qy        243 WIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVY 302
              | |  | |      ::| |:    :| : |::|:|:|  ::|:|||:||    || |||:
Db        230 WDVGNLVS-----KHMNETSHTQGSLRITNISSDDSGKQISCVAENLVGEDQDSVNLTVH 284

Qy        303 YPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKII--------HVEYYQ 354
              : | :  || |       || | |:||| | | | :||  | ||| |         | ||:
Db        285 FAPTITFLESPTSDHHWCIPFTVKGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYH- 343

Qy        355 EGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEP---------FPESTD 405
                  |||  : ||| |||:|||||||  |   : |: ||:  |          :|:
Db        344 ------GCLQLDNPTHMNNGDYTLIAKNEYGKDEKQISAHFMGWPGIDDGANPNYPD--- 394

Qy        406 NFILFDEV--------------SPTPPITVTHKPEEDTFGVSIAVGLAAFA--CVLLVVL 449
                :::::                :  |   || |   :   |   | :|:    | |||:|
Db        395 --VIYEDYGTAANDIGDTTNRSNEIPSTDVTDKTGREHLSVYAVVVIASVVGFC-LLVML 451

Qy        450 FVMINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIP 509
              |::  |  | |||||||| :||| ::|||||||||::|  |||| : ||| |:||||:||
Db        452 FLL--KLARHSKFGMKGPASVISNDDDSASPLHHISNGSNTPSSSEGGPDAVIIGMTKIP 509

Qy        510 VIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLV 569
              ||||||||   ::  ||||:|||||| :|||||||||||||||||||| | :||:||
Db        510 VIENPQYFGITNSQLKPDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLCPEQDKILV 569

Qy        570 AVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFL 629
              ||| ||| :  ||||| |||||||||||||||||||| :|||||||||||||||||||
Db        570 AVKTLKDASDNARKDFHREAELLTNLQHEHIVKFYGVCVEGDPLIMVFEYMKHGDLNKFL 629

Qy        630 RAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGA 689
              |||||||::: :| |     ||  |||||| |||:|||||||||||||||||||||||
Db        630 RAHGPDAVLMAEGNP---PTELTQSQMLHIAQQIAAGMVYLASQHFVHRDLATRNCLVGE 686

Qy        690 NLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTT 749
              ||||||||||||||||||||                ||||||||||||||||||||||
Db        687 NLLVKIGDFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTT 732

Qy        750 ESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQR 809
              |||||| ||:|||||||||||:|||| ||||||||||||:||| ||:|||::|||||||
Db        733 ESDVWSLGVVLWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPQEVYELMLGCWQR 792

Qy        810 EPQQRLNIKEIYKILHALGKATPIYLDILG 839
              ||  | ||| |: :|  | ||:|:||||||
Db        793 EPHMRKNIKGIHTLLQNLAKASPVYLDILG 822
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Search completed: July 12, 2004, 13:45:10
Job time : 58 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:33:15 ; Search time 26 Seconds
(without alignments)
3104.027 Million cell updates/sec

Title: US-09-966-147-6
Perfect score: 4497
Sequence: 1 MDVSLCPAKCSFWRIFLLGS.....IYKILHALGKATPIYLDILG 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4497	100.0	839	1	I73632	neurotrophin-3 rec
2	4381	97.4	825	2	A55178	neurotrophin recep
3	4193	93.2	825	1	A40026	neurotrophin-3 rec
4	3997.5	88.9	852	2	I51259	tyrosine kinase C
5	3707.5	82.4	803	1	S35695	neurotrophin-3 rec
6	2836	63.1	612	2	I73633	gene trkC protein
7	2321	51.6	818	1	S44098	brain-derived neur
8	2287.5	50.9	821	1	S06943	brain-derived neur
9	2287.5	50.9	821	1	A39667	brain-derived neur
10	2277	50.6	822	1	A56853	brain-derived neur
11	2169.5	48.2	525	1	A58674	neurotrophin-3 rec
12	1950	43.4	790	1	TVHUTT	nerve growth facto
13	1913	42.5	799	1	TVRTTB	nerve growth facto
14	1247.5	27.7	503	4	S23741	hypothetical TPR/T
15	1216	27.0	282	2	I51236	brain-derived neur
16	793.5	17.6	871	1	I48696	protein-tyrosine k
17	793.5	17.6	881	1	I48697	protein-tyrosine k
18	788	17.5	520	1	S44099	brain-derived neur
19	773	17.2	474	1	C39667	brain-derived neur
20	773	17.2	476	1	A35104	brain-derived neur
21	773	17.2	476	1	B39667	brain-derived neur
22	763.5	17.0	477	1	I73631	brain-derived neur
23	754	16.8	946	1	A47299	ror-related recept
24	700	15.6	685	1	A48289	neurotrophic recep
25	666	14.8	943	2	B45082	neurotrophic recep
26	653.5	14.5	855	2	S42621	protein-tyrosine k
27	653	14.5	937	2	A45082	neurotrophic recep
28	651.5	14.5	819	2	I48859	tyro 10 receptor k
29	651.5	14.5	1363	2	T43220	insulin-like growt
30	644.5	14.3	168	2	I51297	nerve growth facto
31	630.5	14.0	913	2	A48280	receptor tyrosine
32	629	14.0	910	2	A53137	tyrosine kinase re
33	627.5	14.0	1051	2	A39712	kinase-like protei
34	627.5	14.0	1070	2	JC4593	protein-tyrosine k
35	626.5	13.9	823	2	B35963	protein-tyrosine k
36	625.5	13.9	1382	1	INHUR	insulin receptor p
37	624.5	13.9	650	1	JC1450	fibroblast growth
38	624	13.9	136	2	I51222	neurotropin recept
39	622	13.8	705	2	S51635	fibroblast growth
40	622	13.8	707	2	A38429	keratinocyte growt
41	620	13.8	824	2	S24108	protein-tyrosine k
42	619	13.8	707	2	A54846	fibroblast growth
43	619	13.8	822	2	B54846	fibroblast growth
44	618.5	13.8	802	1	TVHUF4	fibroblast growth
45	618.5	13.8	876	2	A49508	protein-tyrosine k

ALIGNMENTS

RESULT 1
I73632
neurotrophin-3 receptor precursor - human
N;Alternate names: receptor tyrosine kinase trkC
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jun-1999
C;Accession: I73632
R;Shelton, D.L.; Sutherland, J.; Gripp, J.; Camerato, T.; Armanini, M.P.; Phillips, H.S
J. Neurosci. 15, 477-491, 1995
A;Title: Human trks: molecular cloning, tissue distribution, and expression of extracel
A;Reference number: I56557; MUID:95123473; PMID:7823156
A;Accession: I73632
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-839 <RES>
A;Cross-references: GB:S76475; NID:g913721; PIDN:AAB33111.1; PID:g913722
C;Genetics:
A;Gene: GDB:NTRK3; TRKC
A;Cross-references: GDB:127899; OMIM:191316
A;Map position: 15q24-15q25
C;Function:
A;Description: regulation of nervous system development; receptor for neurotrophin-3
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycop
C;Keywords: ATP; autophosphorylation; brain; glycoprotein; growth factor receptor; phos
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-839/Product: neurotrophin-3 receptor #status predicted <MAT>
F;32-436/Domain: extracellular #status predicted <EXT>
F;79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <L
F;437-453/Domain: transmembrane #status predicted <TMN>
F;454-839/Domain: cytosolic #status predicted <CYT>
F;536-831/Domain: protein kinase homology <KIN>
F;544-552/Region: protein kinase ATP-binding motif
F;72,79,133,163,203,218,232,259,267,272,294,375,388/Binding site: carbohydrate (Asn) (c
F;572/Active site: Lys #status predicted
F;709/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict
F;834/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 100.0%; Score 4497; DB 1; Length 839;
Best Local Similarity 100.0%; Pred. No. 1.7e-206;
Matches 839; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
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Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
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Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
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Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
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Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
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Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
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Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
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RESULT 2
A55178
neurotrophin receptor trkC precursor - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Jun-1999
C;Accession: A55178
R;McGregor, L.M.; Baylin, S.B.; Griffin, C.A.; Hawkins, A.L.; Nelkin, B.D.
Genomics 22, 267-272, 1994
A;Title: Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal assignment, a
A;Reference number: A55178; MUID:95104834; PMID:7806211
A;Accession: A55178
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-825 <MCG>
A;Cross-references: GB:U05012; NID:g442389; PIDN:AAA75374.1; PID:g442390
C;Genetics:
A;Gene: GDB:NTRK3
A;Cross-references: GDB:127899; OMIM:191316
A;Map position: 15q24-15q25
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C;Keywords: alternative splicing; ATP; growth factor receptor
F;79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F;536-817/Domain: protein kinase homology <KIN>
F;544-552/Region: protein kinase ATP-binding motif

Query Match 97.4%; Score 4381; DB 2; Length 825;
Best Local Similarity 98.1%; Pred. No. 5.4e-201;
Matches 823; Conservative 2; Mismatches 0; Indels 14; Gaps 1;

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Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
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Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
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Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
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Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
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Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
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Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
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Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
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Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
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Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR--------- 711

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 -----VGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 766

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 825
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RESULT 3
A40026
neurotrophin-3 receptor precursor - pig
N;Alternate names: receptor tyrosine kinase trkC
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 11-Jun-1999

C;Accession: A40026
R;Lamballe, F.; Klein, R.; Barbacid, M.
Cell 66, 967-979, 1991
A;Title: trkC, a new member of the trk family of tyrosine protein kinases, is a receptor
A;Reference number: A40026; MUID:91364178; PMID:1653651
A;Accession: A40026
A;Molecule type: mRNA
A;Residues: 1-825 <LAM>
A;Cross-references: GB:M80800; NID:g164698; PIDN:AAA31130.1; PID:g164699
A;Experimental source: adult brain
C;Function:
A;Description: regulation of nervous system development; receptor for neurotrophin-3
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C;Keywords: ATP; autophosphorylation; brain; glycoprotein; growth factor receptor; phosp
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-825/Product: neurotrophin-3 receptor #status predicted <MAT>
F;32-436/Domain: extracellular #status predicted <EXT>
F;79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F;437-453/Domain: transmembrane #status predicted <TMN>
F;454-825/Domain: cytosolic #status predicted <CYT>
F;536-817/Domain: protein kinase homology <KIN>
F;544-552/Region: protein kinase ATP-binding motif
F;68,72,79,133,163,203,218,232,259,267,272,294,375,388/Binding site: carbohydrate (Asn)
F;572/Active site: Lys #status predicted
F;709/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
F;820/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 93.2%; Score 4193; DB 1; Length 825;
Best Local Similarity 94.2%; Pred. No. 4.6e-192;
Matches 792; Conservative 11; Mismatches 20; Indels 18; Gaps 3;

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Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
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Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:|||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRGLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              |||||:||||:|||||||||||||||||||||||||||||||||||:||||||||||||
Db        181 KLNSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVVTCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              |:|||||||||||||||||||||||||||||||||||||||||||||||| ||||||||:||
Db        301 VHYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKITHVEYYQEGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              |||||||||||||||||  : |||||||||||||||||||||||: | |||||||||
Db        361 GCLLFNKPTHYNNGNYTLNRQEPLGTANQTINGHFLKEPFPESTDNFVSFYEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHIN--HGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538
              |||    |  |  :  ||   ||||||||||||||||||||||||||||||||||||||
Db        481 LHHDQPWHHHTLITGRRAGHS--VIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538

Qy        539 VLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        539 VLKRELGEGAFGKVFLAECYNLSPTKVKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598
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Qy        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658

Qy        659 IASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGN 718
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 IASQICSGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR------- 711

Qy        719 DFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 778
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 -------VGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 764

Qy        779 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 824

Qy        839 G 839
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Db        825 G 825
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RESULT 4
I51259
tyrosine kinase C receptor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 21-Jan-2000
C;Accession: I51259
R;Garner, A.S.; Large, T.H.
Neuron 13, 457-472, 1994
A;Title: Isoforms of the avian TrkC receptor: a novel kinase insertion dissociates tran.
A;Reference number: I51259; MUID:94338700; PMID:8060621
A;Accession: I51259
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-852 <GAR>
A;Cross-references: GB:S74248; NID:g712820; PIDN:AAB31699.1; PID:g712821
C;Genetics:
A;Gene: trkC
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycop
F;79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F;538-844/Domain: protein kinase homology <KIN>

Query Match 88.9%; Score 3997.5; DB 2; Length 852;
Best Local Similarity 87.4%; Pred. No. 9.1e-183;
Matches 745; Conservative 44; Mismatches 50; Indels 13; Gaps 3;

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Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||| ||:|||:||| |:| ||: |||||||||:||||:|||::|||||||||||||
Db          1 MDVSLCPTKCTFWRVFLLWSIWGDYLLSVLACPANCLCSKTDINCKKPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||:|||| :|||||||||||||||::| |||||||||||||:|||:|||||:|||
Db         61 DSGSSNGNTSINITDISRNITSIHIENWKNLQTLNAVDMELYTGLQRLTIRNSGLRNIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              |||||||||||:|| |||||||||||||| | :|:||:| |||||||||:|||||:|||
Db        121 RAFAKNPHLRYIDLSGNRLTTLSWQLFQTLRLFDLRLERNPFNCSCDIRWIQLWQEKGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              | || |:|:| | : : |  |||:|||||||||||||||||||:|||||||||||||||
Db        181 NLQSQQLHCMNLDTAVILLRNMNITQCDLPEISVSHVNLTVREGENAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||| |  | |||||||||||||||||||||||||||||||||| ||||||||||||||| ||
Db        241 VDWTVADLHSINTHQTNLNWTNVHAINLTLVNVTSEDNGFLLTCIAENVVGMSNASVLLT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||:::|||| | ||||| | | ||| |||||||||| |||::|||:|:||:|:|| 
Db        301 VYYPPRILTLEEPVLHLEHCIAFAVHGNPAPTLHWLHNGQVLRETEIIHMEFYQQGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFD--EVSPTPP 418
              |||||||||||||||||::| | ||:||||| ||||::||||||||:     |||||||
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Db        361 GCLLFNKPTHYNNGNYTIVATNQLGSANQTIKGHFLEKPFPESTDNFVSIGDYEVSPTPP 420

Qy        419 ITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSA 478

Db        421 ITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSA 480

Qy        479 SPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538

Db        481 SPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 540

Qy        539 VLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598

Db        541 VLKRELGEGAFGKVFLAECYNLSPTNDKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 600

Qy        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658

Db        601 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 660

Qy        659 IASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLF-NPSG 717

Db        661 IASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYREGPRPKG 720

Qy        718 NDFCIW----------CEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYG 767

Db        721 QLSTAWQRHRLAPPAAATVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYG 780

Qy        768 KQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHAL 827

Db        781 KQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDIMLGCWQREPQQRLNIKEIYKILHAL 840

Qy        828 GKATPIYLDILG 839

Db        841 GKATPIYLDILG 852
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RESULT 5
S35695
neurotrophin-3 receptor precursor - chicken
N;Alternate names: receptor tyrosine kinase trkC
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Gallus gallus (chicken)
C;Date: 10-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 11-Jun-1999
C;Accession: S35695
R;Okazawa, H.; Kamei, M.; Kanazawa, I.
FEBS Lett. 329, 171-177, 1993
A;Title: Molecular cloning and expression of a novel truncated form of chicken trkC.
A;Reference number: S35695; MUID:93359043; PMID:8394830
A;Accession: S35695
A;Molecule type: mRNA
A;Residues: 1-803 <OKA>
A;Cross-references: EMBL:X59669; NID:g416429; PIDN:CAA42202.1; PID:g416430
A;Note: the authors translated the codon AAC for residue 105 as Val, CTG for residue 108
C;Function:
A;Description: regulation of nervous system development; receptor for neurotrophin-3
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C;Keywords: alternative splicing; ATP; autophosphorylation; brain; glycoprotein; growth
otein kinase
F;1-10/Domain: signal sequence #status predicted <SIG>
F;11-803/Product: neurotrophin-3 receptor #status predicted <MAT>
F;11-417/Domain: extracellular #status predicted <EXT>
F;58-82/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;107-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;130-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F;418-434/Domain: transmembrane #status predicted <TMN>
F;435-803/Domain: cytosolic #status predicted <CYT>
F;514-795/Domain: protein kinase homology <KIN>
F;522-530/Region: protein kinase ATP-binding motif
F;47,51,58,142,182,197,211,238,246,251,273,354,367/Binding site: carbohydrate (Asn) (cov
F;550/Active site: Lys #status predicted
F;687/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
F;798/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 82.4%; Score 3707.5; DB 1; Length 803;
Best Local Similarity 84.6%; Pred. No. 5.1e-169;
Matches 703; Conservative 41; Mismatches 50; Indels 37; Gaps 5;

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Qy         13 WRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQDSGNSNGNANIN 72

Db          6 WRIF--------------ASDRLKVLFKTDINCKKPDDGNLFPLLEGQDSGSSNGNTSIN 51

Qy         73 ITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYI 132

Db         52 ITDISRNITSIHIENWKNLQTLNAVDMELYTGLQRLTIRNSGLRNIQPRAFGKNPHLRYI 111

Qy        133 NLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINA 192

Db        112 DLSGNRLTTLSWQLFQTLRLFDLRLERNPFNCSCDIRWIQLWQEKGEANLQSQQLHCMNL 171

Qy        193 DGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSIN 252

Db        172 DTAVILLRNMNITQCDLPEISVSHVNLTVREGENAVITCNGSGSPLPDVDWTVADLHSIN 231

Qy        253 THQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEE 312

Db        232 THQTNLNWTNVHAINLTLVNVTSEDNGFLLTCIAENVVGMSNASVLLTVYYPPRILTLEE 291

Qy        313 PELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYN 372

Db        292 PVLHLEHCIAFAVHGNPAPTLHWLHNGQVLRETEIIHMEFYQQGEVSEGCLLFNKPTHYN 351

Qy        373 NGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFD--EVSPTPPITVTHKPEEDTF 430

Db        352 NGNYTIVATNQLGSANQTIKGHFLEKPFPESTDNFVSIGDYEVSPTPPITVTHKPEEDTF 411

Qy        431 GVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITT 490

Db        412 GVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSAA-----THTSTT 466

Qy        491 PSSL--DAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGA 548

Db        467 DTRFVTDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGA 526

Qy        549 FGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCG 608

Db        527 FGKVFLAECYNLSPTNDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCG 586

Qy        609 DGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMV 668

Db        587 DGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMV 646

Qy        669 YLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGG 728

Db        647 YLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR--------------VGG 692

Qy        729 HTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRV 788

Db        693 HTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRV 752

Qy        789 LERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839

Db        753 LERPRVCPKEVYDIMLGCCQREPQQRLNIKEIYKILHALGKATPIYLDILG 803
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RESULT 6
I73633
gene trkC protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: I73633
R;Shelton, D.L.; Sutherland, J.; Gripp, J.; Camerato, T.; Armanini, M.P.; Phillips, H.S.
J. Neurosci. 15, 477-491, 1995
A;Title: Human trks: molecular cloning, tissue distribution, and expression of extracell
A;Reference number: I56557; MUID:95123473; PMID:7823156
A;Accession: I73633
A;Status: preliminary; translated from GB/EMBL/DDBJ

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A;Molecule type: mRNA
A;Residues: 1-612 <RES>
A;Cross-references: GB:S76476; NID:g913723; PIDN:AAB33112.1; PID:g913724
C;Genetics:
A;Gene: trkC
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
F;79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

  Query Match             63.1%;  Score 2836;  DB 2;  Length 612;
  Best Local Similarity   99.8%;  Pred. No. 9.3e-128;
  Matches  529;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYV 530
              |||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTWV 530


RESULT 7
S44098
brain-derived neurotrophic factor receptor precursor - chicken
N;Alternate names: receptor tyrosine kinase trkB
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999
C;Accession: S59939; S42175; S44098
R;Vinh, N.Q.; Erdmann, K.S.; Heumann, R.
Gene 149, 383-384, 1994
A;Title: Cloning and sequence analysis of a cDNA encoding a novel truncated form of the
A;Reference number: S59938; MUID:95047511; PMID:7959025
A;Accession: S59939
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-818 <VI2>
A;Cross-references: EMBL:X77251; NID:g563881; PIDN:CAA54468.1; PID:g472934
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
R;Dechant, G.; Biffo, S.; Okazawa, H.; Kolbeck, R.; Pottgiesser, J.; Barde, Y.A.
Development 119, 545-558, 1993
A;Title: Expression and binding characteristics of the BDNF receptor chick trkB.
A;Reference number: S42175; MUID:94116452; PMID:8287802
A;Accession: S42175
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-818 <DEC>
A;Cross-references: EMBL:X74109; NID:g407798; PIDN:CAA52210.1; PID:g407799
C;Genetics:
A;Gene: trkB
C;Function:
A;Description: regulation of nervous system development; receptor for brain-derived neu
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycop
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
inase
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-818/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>
F;32-432/Domain: extracellular #status predicted <EXT>
F;66-90/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;91-114/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;115-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;138-149/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <L
F;433-449/Domain: transmembrane #status predicted <TMN>
F;450-818/Domain: cytosolic #status predicted <CYT>
F;532-810/Domain: protein kinase homology <KIN>
F;540-548/Region: protein kinase ATP-binding motif
F;66,94,120,199,204,253,287,324,337,349,408/Binding site: carbohydrate (Asn) (covalent)
F;568/Active site: Lys #status predicted
F;702/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict
F;813/Binding site: phosphate (Tyr) (covalent) #status predicted

  Query Match             51.6%;  Score 2321;  DB 1;  Length 818;
  Best Local Similarity   53.8%;  Pred. No. 3.6e-103;
  Matches  463;  Conservative  120;  Mismatches  193;  Indels   84;  Gaps   15;

Qy          5 LCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDG-NLFPLLEGQDSG 63
              ||      ||               | |||:| ||   | |  |  |   ||: :
Db         18 LCCLVLGCWR------------GALGCPASCRCSSWRIWCSEPVPGITSFPVPQRSTED 64

Qy         64 NSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAF 123
              :              |:| |:| | | | ::|  ::  | ||: ||: :|||| :  :||
Db         65 D-------------NVTEIYIANQRKLESINDNEVGFYVGLKNLTVVDSGLRFVSRQAF 110

Qy        124 AKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLN 183
              || :|:|||| |:|::|| : |: | | :| |  | | |||:| |:: :||  :
Db        111 VKNINLQYINLSRNKLSSLSKKPFRHLGLSDLILVDNPFKCSCEIMWIKKFQET-KFYTE 169

Qy        184 SQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDW 243
              :|::||:: :  :: |  | :  ||||  ::|: |:|| || :  :  |: :| | |:| |
Db        170 AQDIYCVDDNNKRIALMDMKVPNCDLPSANLSNYNITVVEGKSITLYCDTTGGPPPNVSW 229

Qy        244 IVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYY 303
              ::| |  :: |:::   |: :  :||: ||:| |:|  ::|:|||:||     |  |||::
Db        230 VLTNL--VSNHESD---TSKNPASLTIKNVSSMDSGLWISCVAENIVGEVQTSAELTVFF 284

Qy        304 PPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKI----IHV----EYYQE 355
              | :  :| |       || | |:||| ||| | : |  | ||:     |||    ||:
Db        285 APNITFIESPTPDHHWCIPFTVKGNPKPTLQWFYEGAILNESEYICTKIHVINQSEYH-- 342

Qy        356 GEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFP------------E 402
                 |||  : ||| ||| |||:||| |   : :: ||:  |                |
Db        343 -----GCLQLDNPTHLNNGAYTLLAKNEYGEDEKRVDAHFMSVPGDGSGPIVDPDVYEYE 397

Qy        403 STDNFILFDEVSPTPPIT---VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRR 459
              :| |  | |  : :  ||   |::|  ||:  | : ||:||  |  ||:: ::: |:||
Db        398 TTPN-DLGDTTNNSNQITSPDVSNKENEDSITVYVVVGIAALVCTGLVIMLIIL-KFGRH 455

Qy        460 SKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQ 519
              |||||||| :||| ::|||||||||::|  |||| : ||| |:||||:|||||||||||
Db        456 SKFGMKGPSSVISNDDDSASPLHHISNGSNTPSSSEGGPDAVIIGMTKIPVIENPQYFGI 515

Qy        520 GHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTL 579
               ::  ||||:|||||| :|||||||||||||||||||| | :||:|||| ||| :
Db        516 TNSQLKPDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLCPEQDKILVAVKTLKDASD 575

Qy        580 AARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMIL 639
              |||||  |||||||||||||||||||| :|||||||||||||||||||||||||:::
Db        576 NARKDFHREAELLTNLQHEHIVKFYGVCVEGDPLIMVFEYMKHGDLNKFLRAHGPDAVLM 635
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Qy        640 VDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFG 699
Db        636 AEG---NRPAELTQSQMLHIAQQIAAGMVYLASQHFVHRDLATRNCLVGENLLVKIGDFG 692

Qy        700 MSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVI 759
Db        693 MSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTESDVWSLGVV 738

Qy        760 LWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKE 819
Db        739 LWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPKEVYDLMLGCWQREPHMRLNIKE 798

Qy        820 IYKILHALGKATPIYLDILG 839
Db        799 IHSLLQNLAKASPVYLDILG 818
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RESULT 8
S06943
brain-derived neurotrophic factor receptor precursor - mouse
N;Alternate names: receptor tyrosine kinase trkB
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Mus musculus (house mouse)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 11-Jun-1999
C;Accession: S06943
R;Klein, R.; Parada, L.F.; Coulier, F.; Barbacid, M.
EMBO J. 8, 3701-3709, 1989
A;Title: trkB, a novel tyrosine protein kinase receptor expressed during mouse neural de
A;Reference number: S06943; MUID:90059970; PMID:2555172
A;Accession: S06943
A;Molecule type: mRNA
A;Residues: 1-821 <KLE>
A;Cross-references: EMBL:X17647; NID:g55505; PIDN:CAA35636.1; PID:g55506
C;Genetics:
A;Gene: trkB
C;Function:
A;Description: regulation of nervous system development; receptor for brain-derived neur
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
inase
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-821/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>
F;32-434/Domain: extracellular #status predicted <EXT>
F;67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F;435-451/Domain: transmembrane #status predicted <TMN>
F;452-821/Domain: cytosolic #status predicted <CYT>
F;535-813/Domain: protein kinase homology <KIN>
F;543-551/Region: protein kinase ATP-binding motif
F;67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Asn) (covale
F;571/Active site: Lys #status predicted
F;706/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
F;816/Binding site: phosphate (Tyr) (covalent) #status predicted

  Query Match 50.9%; Score 2287.5; DB 1; Length 821;
  Best Local Similarity 54.0%; Pred. No. 1.4e-101;
  Matches 466; Conservative 110; Mismatches 206; Indels 81; Gaps 15;

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Qy          7 PAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDSGNS 65
Db         10 PAMARLWGLCLL---VLGFWRASLACPTSCKCSSARIWCTEPSPGIVAFPRLEP------ 60

Qy         66 NGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAK 125
Db         61 ------NSVD-PENITEILIANQKRLEIINEDDVEAYVGLRNLTIVDSGLKFVAYKAFLK 113

Qy        126 NPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQ 185
Db        114 NSNLRHINFTRNKLTSLSRRHFRHLDLSDLILTGNPFTCSCDIMWLKTLQET-KSSPDTQ 172

Qy        186 NLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIV 245
Db        173 DLYCLNESSKNMPLANLQIPNCGLPSARLAAPNLTVEEGKSVTLSCSVGGDPLPTLYWDV 232

Qy        246 TGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPP 305
Db        233 GNLVS-----KHMNETSHTQGSLRITNISSDDSGKQISCVAENLVGEDQDSVNLTVHFAP 287

Qy        306 RVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKII--------HVEYYQEGE 357
Db        288 TITFLESPTSDHHWCIPFTVRGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYH---- 343

Qy        358 ISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEP---------FPESTDNFI 408
Db        344 ---GCLQLDNPTHMNNGDYTLMAKNEYGKDERQISAHFMGRPGVDYETNPNYPE-----V 395

Qy        409 LFDE-VSPTPPITVTHK----PEEDTFGVSIAVGLAAFACVLL-------VVLFVMINKY 456
Db        396 LYEDWTTPTDIGDTTNKSNEIPSTDVADQSNREHLSVYAVVVIASVVGFCLLVMLLLKL 455

Qy        457 GRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQY 516
Db        456 ARHSKFGMKGPASVISNDDDSASPLHHISNGSNTPSSSEGGPDAVIIGMTKIPVIENPQY 515

Qy        517 FRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKD 576
Db        516 FGITNSQLKPDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLCPEQDKILVAVKTLKD 575

Qy        577 PTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDA 636
Db        576 ASDNARKDFHREAELLTNLQHEHIVKFYGVCVEGDPLIMVFEYMKHGDLNKFLRAHGPDA 635

Qy        637 MILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIG 696
Db        636 VLMAEGNP---PTELTQSQMLHIAQQIAAGMVYLASQHFVHRDLATRNCLVGENLLVKIG 692

Qy        697 DFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSF 756
Db        693 DFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTESDVWSL 738

Qy        757 GVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLN 816
Db        739 GVVLWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPQEVYELMLGCWQREPHTRKN 798

Qy        817 IKEIYKILHALGKATPIYLDILG 839
Db        799 IKSIHTLLQNLAKASPVYLDILG 821
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RESULT 9
A39667
brain-derived neurotrophic factor receptor precursor - rat
N;Alternate names: receptor tyrosine kinase trkB.FL
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 11-Jun-1999
C;Accession: A39667
R;Middlemas, D.S.; Lindberg, R.A.; Hunter, T.
Mol. Cell. Biol. 11, 143-153, 1991
A;Title: trkB, a neural receptor protein-tyrosine kinase: evidence for a full-length and
A;Reference number: A39667; MUID:91094826; PMID:1846020
A;Accession: A39667
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-821 <MID>
A;Cross-references: GB:M55291; NID:g207473; PIDN:AAA42279.1; PID:g207474
C;Function:
A;Description: regulation of nervous system development; receptor for brain-derived neur
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
inase
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-821/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>

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F;32-434/Domain: extracellular #status predicted <EXT>
F;67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F;435-451/Domain: transmembrane #status predicted <TMN>
F;452-821/Domain: cytosolic #status predicted <CYT>
F;535-813/Domain: protein kinase homology <KIN>
F;543-551/Region: protein kinase ATP-binding motif
F;67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Asn) (covale
F;571/Active site: Lys #status predicted
F;705/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
F;816/Binding site: phosphate (Tyr) (covalent) #status predicted

  Query Match           50.9%;  Score 2287.5;  DB 1;  Length 821;
  Best Local Similarity  54.0%;  Pred. No. 1.4e-101;
  Matches  468;  Conservative  106;  Mismatches  204;  Indels   89;  Gaps   16;

Qy          7 PAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDSGNS 65
              ||    | : ||    | :  : |||| :| || | |  |  | : || ||
Db         10 PAMARLWGLCLL---VLGFWRASLACPMSCKCSTTRIWCTEPSPGIVAFPRLEP------ 60

Qy         66 NGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAK 125
                |  |   ||| | | : |  :|  |:| | ||: ||| :|||: :  :|| |
Db         61 ------NSID-PENITEILIANQKRLEIINEDDVEAYVGLKNLTIVDSGLKFVAYKAFLK 113

Qy        126 NPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQ 185
              | :||:|| : |:||:|| : |: | | :| |  | | ||||| |::  ||  ::  ::|
Db        114 NGNLRHINFTRNKLTSLSRRHFRHLDLSDLILTGNPFTCSCDIMWLKTLQET-KSSPDTQ 172

Qy        186 NLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIV 245
              :|||:|       ||  : |  | ||    ::  |||| || :  |:|:  | ||| : | |
Db        173 DLYCLNESSKNTPLANLQIPNCGLPSARLAAPNLTVEEGKSVTISCSVGGDPLPTLYWDV 232

Qy        246 TGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPP 305
              | |       ::| |:    :| : |::|:|:|  ::|:|||:||    || |||:: |
Db        233 GNLVS-----KHMNETSHTQGSLRITNISSDDSGKQISCVAENLVGEDQDSVNLTVHFAP 287

Qy        306 RVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKII--------HVEYYQEGE 357
              :  || |       || | ||||| | | | :||  | ||| |         | ||:
Db        288 TITFLESPTSDHHWCIPFTVRGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYH---- 343

Qy        358 ISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEP---------FPESTDNFI 408
                |||  : ||| |||:|||:|||  |   : |: ||:  |          :||     :
Db        344 ---GCLQLDNPTHMNNGDYTLMAKNEYGKDERQISAHFMGRPGVDYETNPNYPE-----V 395

Qy        409 LFDE-VSPTPPITVTHKPEE---------------DTFGVSIAVGLAAFACVLLVVLFVM 452
              |:::  :||      |:|  |                : | :   :  | |:|:::| :
Db        396 LYEDWTTPTDIGDTTNKSNEIPSTDVADQTNREHLSVYAVVVIASVVGF-CLLVMLLLL- 453

Qy        453 INKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIE 512
              |  | |||||||| :||| ::|||||||||::|  |||| : ||| |:||||:|||||
Db        454 --KLARHSKFGMKGPASVISNDDDSASPLHHISNGSNTPSSSEGGPDAVIIGMTKIPVIE 511

Qy        513 NPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVK 572
              |||||   ::  ||||:|||||| :|||||||||||||||||||| | :||:|||||
Db        512 NPQYFGITNSQLKPDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLCPEQDKILVAVK 571

Qy        573 ALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAH 632
              |||  : ||||| |||||||||||||||||||| :|||||||||||||||||||||||||
Db        572 TLKDASDNARKDFHREAELLTNLQHEHIVKFYGVCVEGDPLIMVFEYMKHGDLNKFLRAH 631

Qy        633 GPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLL 692
              ||||::: :| |      ||  |||||||| |||:|||||||||||||||||||||||| |||
Db        632 GPDAVLMAEGNP---PTELTQSQMLHIAQQIAAGMVYLASQHFVHRDLATRNCLVGENLL 688

Qy        693 VKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESD 752
              ||||||||||||||||||                 |||||||||||||||||||||||||
Db        689 VKIGDFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTESD 734

Qy        753 VWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQ 812
              ||| ||:|||||||||||:|||| ||||||||||||:||| ||:|||::|||||||||
Db        735 VWSLGVVLWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPQEVYELMLGCWQREPH 794

Qy        813 QRLNIKEIYKILHALGKATPIYLDILG 839
                | ||| |: :|  | ||:|:||||||
Db        795 TRKNIKNIHTLLQNLAKASPVYLDILG 821


RESULT 10
A56853
brain-derived neurotrophic factor receptor precursor - human
N;Alternate names: receptor tyrosine kinase trkB
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 11-Jun-1999
C;Accession: A56853; I56557
R;Nakagawara, A.; Liu, X.G.; Ikegaki, N.; White, P.S.; Yamashiro, D.J.; Nycum, L.M.; Bi
Genomics 25, 538-546, 1995
A;Title: Cloning and chromosomal localization of the human TRK-B tyrosine kinase recept
A;Reference number: A56853; MUID:95309922; PMID:7789988
A;Accession: A56853
A;Molecule type: mRNA
A;Residues: 1-822 <NAK>
A;Cross-references: GB:U12140; NID:g525313; PIDN:AAC51371.1; PID:g530791
R;Shelton, D.L.; Sutherland, J.; Gripp, J.; Camerato, T.; Armanini, M.P.; Phillips, H.S
J. Neurosci. 15, 477-491, 1995
A;Title: Human trks: molecular cloning, tissue distribution, and expression of extracell
A;Reference number: I56557; MUID:95123473; PMID:7823156
A;Accession: I56557
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-822 <SHE>
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A;Gene: GDB:NTRK2; trkB
A;Cross-references: GDB:127898; OMIM:600456
A;Map position: 9q22.1-9q22.1
C;Function:
A;Description: regulation of nervous system development; receptor for brain-derived neur
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
inase
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-822/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>
F;32-435/Domain: extracellular #status predicted <EXT>
F;67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F;436-452/Domain: transmembrane #status predicted <TMN>
F;453-822/Domain: cytosolic #status predicted <CYT>
F;536-814/Domain: protein kinase homology <KIN>
F;544-552/Region: protein kinase ATP-binding motif
F;67,95,121,178,205,241,254,280,325,338,350,412/Binding site: carbohydrate (Asn) (covalc
F;572/Active site: Lys #status predicted
F;706/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
F;817/Binding site: phosphate (Tyr) (covalent) #status predicted

  Query Match           50.6%;  Score 2277;  DB 1;  Length 822;
  Best Local Similarity  53.7%;  Pred. No. 4.5e-101;
  Matches  467;  Conservative  110;  Mismatches  199;  Indels   94;  Gaps   18;

Qy          7 PAKCSFWRIFLLGSVWLDYVG---SVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDS 62
              ||    |     |  ||  ||   :  ||| :| || : | |  |  | : || ||
Db         10 PAMARLW-----GFCWL-VVGFWRAAFACPTSCKCSASRIWCSDPSPGIVAFPRLEP--- 60

Qy         63 GNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRA 122
                |  |   ||| | | : |  :|  |:| | ||: ||| :|||: :  :|
Db         61 ---------NSVD-PENITEIFIANQKRLEIINEDDVEAYVGLRNLTIVDSGLKFVAHKA 110

Qy        123 FAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKL 182
              | || :|::|| : |:||:|| : |: | | || |  | | ||||| |::  ||  ::
Db        111 FLKNSNLQHINFTRNKLTSLSRKHFRHLDLSELILVGNPFTCSCDIMWIKTLQE-AKSSP 169

Qy        183 NSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVD 242
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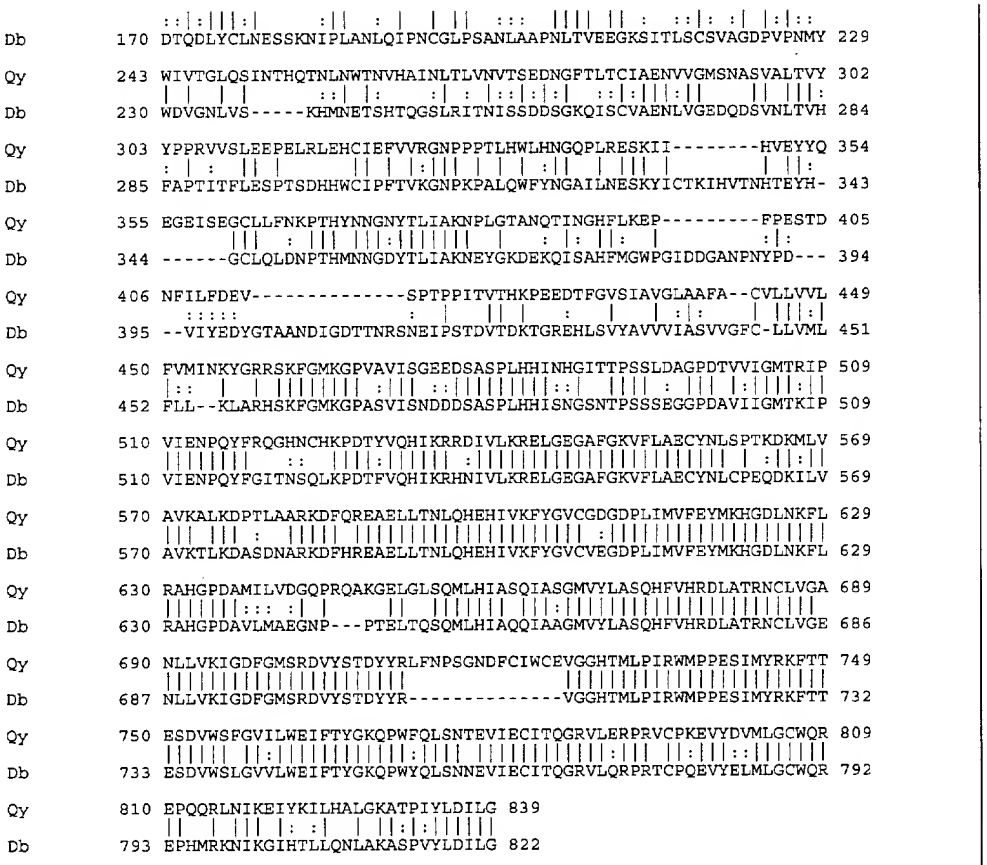
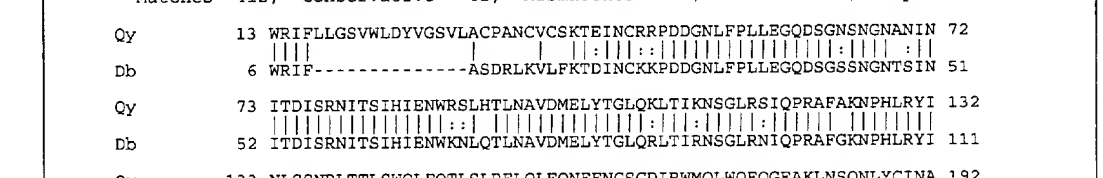
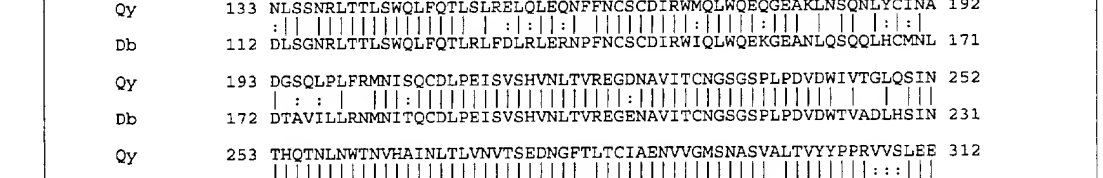


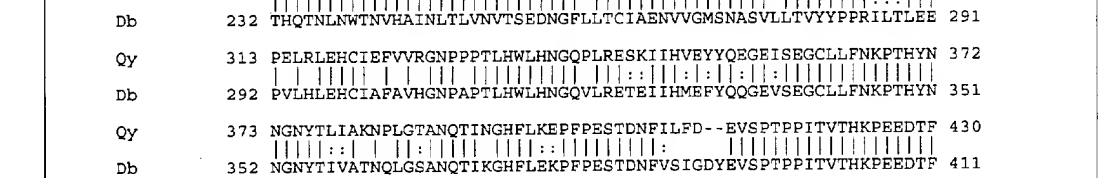
RESULT 11
A58674
neurotrophin-3 receptor precursor, short splice form - chicken
N;Alternate names: truncated receptor tyrosine kinase trkC
C;Species: Gallus gallus (chicken)
C;Date: 19-Nov-1997 #sequence_revision 21-Nov-1997 #text_change 21-Nov-1997
C;Accession: A58674
R;Okazawa, H.; Kamei, M.; Kanazawa, I.
FEBS Lett. 329, 171-177, 1993
A;Title: Molecular cloning and expression of a novel truncated form of chicken trkC.
A;Reference number: S35695; MUID:93359043; PMID:8394830
A;Accession: A58674
A;Molecule type: mRNA
A;Residues: 1-525 <OKA>
A;Note: the authors translated the codon AAC for residue 105 as Val, CTG for residue 108
C;Comment: This form of the receptor is missing the protein kinase domain.
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C;Keywords: alternative splicing; brain; glycoprotein; growth factor receptor; tandem re
F;1-10/Domain: signal sequence #status predicted <SIG>
F;11-525/Product: neurotrophin-3 receptor, short form #status predicted <MAT>
F;11-417/Domain: extracellular #status predicted <EXT>
F;58-82/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;107-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;130-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR

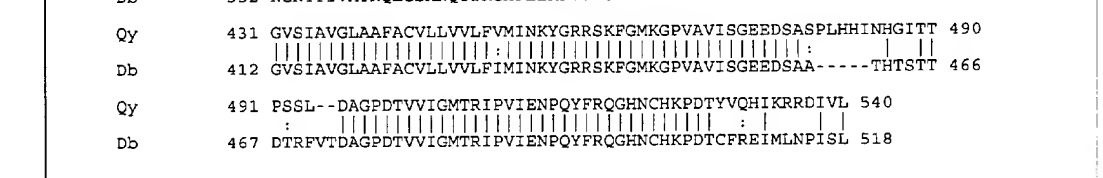
F;418-434/Domain: transmembrane #status predicted <TMN>
F;435-525/Domain: cytosolic #status predicted <CYT>
F;47,51,58,142,182,197,211,238,246,251,273,354,367/Binding site: carbohydrate (Asn) (cov

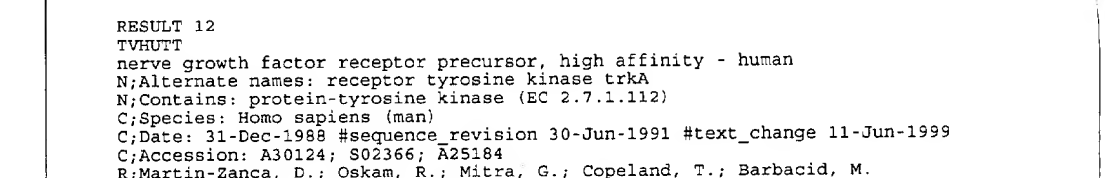
Query Match 48.2%; Score 2169.5; DB 1; Length 525;
Best Local Similarity 77.4%; Pred. No. 3.5e-96;
Matches 412; Conservative 41; Mismatches 56; Indels 23; Gaps 4;

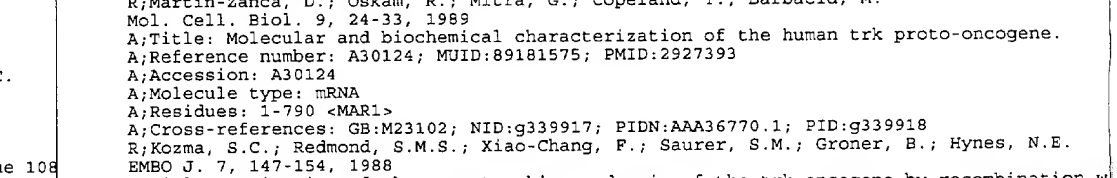


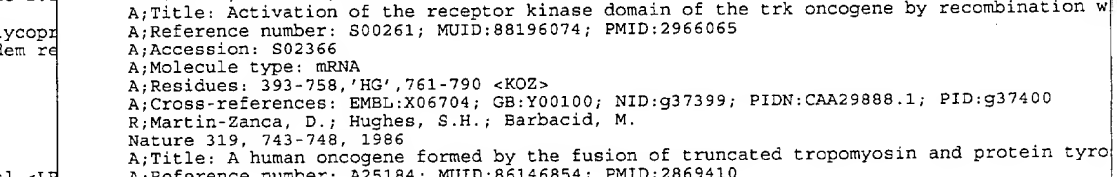












RESULT 12
TVHUTT
nerve growth factor receptor precursor, high affinity - human
N;Alternate names: receptor tyrosine kinase trkA
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 11-Jun-1999
C;Accession: A30124; S02366; A25184
R;Martin-Zanca, D.; Oskam, R.; Mitra, G.; Copeland, T.; Barbacid, M.
Mol. Cell. Biol. 9, 24-33, 1989
A;Title: Molecular and biochemical characterization of the human trk proto-oncogene.
A;Reference number: A30124; MUID:89181575; PMID:2927393
A;Accession: A30124
A;Molecule type: mRNA
A;Residues: 1-790 <MAR1>
A;Cross-references: GB:M23102; NID:g339917; PIDN:AAA36770.1; PID:g339918
R;Kozma, S.C.; Redmond, S.M.S.; Xiao-Chang, F.; Saurer, S.M.; Groner, B.; Hynes, N.E.
EMBO J. 7, 147-154, 1988
A;Title: Activation of the receptor kinase domain of the trk oncogene by recombination w
A;Reference number: S00261; MUID:88196074; PMID:2966065
A;Accession: S02366
A;Molecule type: mRNA
A;Residues: 393-758,'HG',761-790 <KOZ>
A;Cross-references: EMBL:X06704; GB:Y00100; NID:g37399; PIDN:CAA29888.1; PID:g37400
R;Martin-Zanca, D.; Hughes, S.H.; Barbacid, M.
Nature 319, 743-748, 1986
A;Title: A human oncogene formed by the fusion of truncated tropomyosin and protein tyro
A;Reference number: A25184; MUID:86146854; PMID:2869410

```
A;Accession: A25184
A;Molecule type: mRNA
A;Residues: 393-762,'SNATASRMCTPGCKPWPRHLLSTWMSWARGPAQGLGVVSRNTGACPQHPP' <MAR2>
A;Cross-references: EMBL:X03541; NID:g37402; PIDN:CAA27243.1; PID:g37403
A;Note: the difference at the carboxyl end is due to a frameshift
C;Comment: The proto-oncogene trkA is activated by gene fusion. The amino end of several
C;Genetics:
A;Gene: GDB:NTRK1; TRK
A;Cross-references: GDB:127897; OMIM:191315
A;Map position: 1q21-1q22
C;Function:
A;Description: regulation of nervous system development; receptor for nerve growth facto
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprote
ecific protein kinase
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-790/Product: nerve growth factor receptor, high-affinity #status predicted <MAT>
F;33-415/Domain: extracellular #status predicted <EXT>
F;67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F;416-432/Domain: transmembrane #status predicted <TMN>
F;433-790/Domain: cytosolic #status predicted <CYT>
F;502-782/Domain: protein kinase homology <KIN>
F;510-518/Region: protein kinase ATP-binding motif
F;67,95,121,188,202,253,262,281,318,323,338,358,395/Binding site: carbohydrate (Asn) (co
F;538/Active site: Lys #status predicted
F;674/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
F;785/Binding site: phosphate (Tyr) (covalent) #status predicted

  Query Match             43.4%;  Score 1950;  DB 1;  Length 790;
  Best Local Similarity   49.7%;  Pred. No. 1.5e-85;
  Matches  419;  Conservative  103;  Mismatches  229;  Indels   92;  Gaps   17;

Qy         22 WLDYVGSVLA-----------CP-ANCVCSKTEINCRRPDDGNLFPL--LEGQDSGNSNG 67
Db         15 WAAGPGSLLAWLILASAGAAPCPDACCPHGSSGLRCTR--DGALDSLHHLPG-------- 64

Qy         68 NANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNP 127
Db         65 ---------AENLTELYIENQQHLQHLELRDLRGLGELRNLTIVKSGLRFVAPDAFHFTP 115

Qy        128 HLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNL 187
Db        116 RLSRLNLSFNALESLSWKTVQGLSLQELVLSGNPLHCSCALRWLQRWEEEGLGGVPEQKL 175

Qy        188 YCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTG 247
Db        176 QC----HGQGPLAHMPNASCGVPTLKVQVPNASVDVGDDVLLRCQVEGRGLEQAGWILTE 231

Qy        248 LQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRV 307
Db        232 LEQ---SATVMKSGGLPSLGLTLANVTSDLNRKNLTCWAENDVGRAEVSVQVNVSFPASV 288

Qy        308 VSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEG---EISEGCLL 364
Db        289 QLHTAVEMH-HWSIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCLR 347

Qy        365 FNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPITVTH- 423
Db        348 LNQPTHVNNGNYTLLAANPFGQASASIMAAFMDNPF-----------EFNPEDPIPDTNS 396

Qy        424 -------KPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEED 476
Db        397 TSGDPVEKKDETPFGVSVAVGLAVFACLFLSTLLLVLNKCGRRNKFGINRP-AVLAPEDG 455

Qy        477 SASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRR 536
Db        456 LAMSLHFMTLGGSSLSPTE-GKGSGLQG----HIIENPQYF--------SDACVHHIKRR 502

Qy        537 DIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQ 596
Db        503 DIVLKWELGEGAFGKVFLAECHNLLPEQDKMLVAVKALKEASESARQDFQREAELLTMLQ 562

Qy        597 HEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQM 656
Db        563 HQHIVRFFGVCTEGRPLLMVFEYMRHGDLNRFLRSHGPDAKLLAGGED-VAPGPLGLGQL 621

Qy        657 LHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPS 716
Db        622 LAVASQVAAGMVYLAGLHFVHRDLATRNCLVGQGLVVKIGDFGMSRDIYSTDYYR----- 676

Qy        717 GNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSN 776
Db        677 ---------VGGRTMLPIRWMPPESILYRKFTTESDVWSFGVVLWEIFTYGKQPWYQLSN 727

Qy        777 TEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLD 836
Db        728 TEAIDCITQGRELERPRACPPEVYAIMRGCWQREPQQRHSIKDVHARLQALAQAPPVYLD 787

Qy        837 ILG 839
Db        788 VLG 790


RESULT 13
TVRTTB
nerve growth factor receptor precursor, high affinity - rat
N;Alternate names: receptor tyrosine kinase trkA
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2000
C;Accession: A41981
R;Meakin, S.O.; Suter, U.; Drinkwater, C.C.; Welcher, A.A.; Shooter, E.M.
Proc. Natl. Acad. Sci. U.S.A. 89, 2374-2378, 1992
A;Title: The rat trk protooncogene product exhibits properties characteristic of the slo
A;Reference number: A41981; MUID:92196121; PMID:1312719
A;Accession: A41981
A;Molecule type: mRNA
A;Residues: 1-799 <MEA>
A;Cross-references: GB:M85214; NID:g207481; PIDN:AAA42286.1; PID:g207482
A;Note: sequence extracted from NCBI backbone (NCBIN:88433, NCBIP:88434)
A;Note: in Genbank entry RATTRKPREC, release 113.0, the source is designated as Rattus r
C;Comment: The proto-oncogene trkA is activated by gene fusion. The amino end of several
C;Function:
A;Description: regulation of nervous system development; receptor for nerve growth facto
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprote
ecific protein kinase
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-799/Product: nerve growth factor receptor, high-affinity #status predicted <MAT>
F;33-424/Domain: extracellular #status predicted <EXT>
F;67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F;92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F;116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F;425-441/Domain: transmembrane #status predicted <TMN>
F;442-799/Domain: cytosolic #status predicted <CYT>
F;511-791/Domain: protein kinase homology <KIN>
F;519-527/Region: protein kinase ATP-binding motif
F;67,121,190,204,255,264,320,325,341,361,404/Binding site: carbohydrate (Asn) (covalent)
F;547/Active site: Lys #status predicted
F;683/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte
F;794/Binding site: phosphate (Tyr) (covalent) #status predicted

  Query Match             42.5%;  Score 1913;  DB 1;  Length 799;
  Best Local Similarity   48.2%;  Pred. No. 8.4e-84;
  Matches  403;  Conservative  115;  Mismatches  230;  Indels   88;  Gaps   14;

Qy         29 VLACPANCVCSKT-------EINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNIT 81
Db         27 MLACACAASCRETCCPVGPSGLRCTRAGTLNTLRGLRG----------------AGNLT 69

Qy         82 SIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTT 141
```

```
Db          70 ELYVENQRDLQRLEFEDLQGLGELRSLTIVKSGLRFVAPDAFHFTPRLSHLNLSSNALES 129

Qy         142 LSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFR 201
               |||:  | |||::| |   |  :||| : |:| |:::    : :| |    :    |||
Db         130 LSWKTVQGLSLQDLTLSGNPLHCSCALLWLQRWEQEDLCGVYTQKLQGSGSGDQFLPLGH 189

Qy         202 MNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWT 261
               |   | :| : :   | :|  ||:  : |   |  |   |||:| |:   | : :
Db         190 NN--SCGVPSVKIQMPNDSVEVGDDVFLQCQVEGQALQQADWILTELEGTATMKKS---G 244

Qy         262 NVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCI 321
               :: :: |||||||: |   :|| ||| || :  || ::| :|   | | :   :   ||
Db         245 DLPSLGLTLVNVTSDLNKKNVTCWAENDVGRAEVSVQVSVSFPAS-VHLGKAVEQHHWCI 303

Qy         322 EFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE----GCLLFNKPTHYNNGNYT 377
               | | | | |:| |  ||  | |:  |  :: :    :|    |||  |:||| ||||||
Db         304 PFSVDGQPAPSLRWFFNGSVLNETSFIFTQFLESALTNETMRHGCLRLNQPTHVNNGNYT 363

Qy         378 LIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPITVTHKP------------ 425
               |:| || | |  :|   |:  ||           | :|  || |:  |
Db         364 LLAANPYGQAAASIMAAFMDNPF-----------EFNPEDPIPVSFSPVDTNSTSRDPVE 412

Qy         426 --EEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASPLHH 483
                 :|  ||||:|||||  | : |  | :::|| |:|||||:  | ||:: |:  |  ||
Db         413 KKDETPFGVSVAVGLAVSAALFLSALLLVLNKCGQRSKFGINRP-AVLAPEDGLAMSLHF 471

Qy         484 INHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRE 543
               :  | :: |  : |  : : |     ::|||||          || | ||||:||:|| |
Db         472 MTLGGSSLSPTE-GKGSGLQG----HIMENPQYF--------SDTCVHHIKRQDIILKWE 518

Qy         544 LGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHIVKF 603
               |||||||||||||||   :||||||||||: :  ||:|| |||||| |||:|||:|
Db         519 LGEGAFGKVFLAECYNLLNDQDKMLVAVKALKETSENARQDFHREAELLTMLQHQHIVRF 578

Qy         604 YGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIASQI 663
               :||| :| ||:||||||:|||||:|||:|||| :|  |:  | | ||| |:| :|||:
Db         579 FGVCTEGGPLLMVFEYMRHGDLNRFLRSHGPDAKLLAGGED-VAPGPLGLGQLLAVASQV 637

Qy         664 ASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIW 723
               |:|||||| ||||||||||||||  |:|||||||||:|||||||
Db         638 AAGMVYLASLHFVHRDLATRNCLVGQGLVVKIGDFGMSRDIYSTDYYR------------ 685

Qy         724 CEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECI 783
                  ||| |||||||||||||:||||:||||||||||:||||||||||:||||||  ||||
Db         686 --VGGRTMLPIRWMPPESILYRKFSTESDVWSFGVVLWEIFTYGKQPWYQLSNTEAIECI 743

Qy         784 TQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
               |||| ||||| || :|| :| |||||||||||::|:::  | || :| | |||:||
Db         744 TQGRELERPRACPPDVYAIMRGCWQREPQQRLSMKDVHARLQALAQAPPSYLDVLG 799
```

RESULT 14
S23741
hypothetical TPR/TRK mutant fusion protein - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Sep-1997 #text_change 14-May-1999
C;Accession: S23741
R;Greco, A.; Pierotti, M.A.; Bongarzone, I.; Pagliardini, S.; Lanzi, C.; Della Porta, G.
Oncogene 7, 237-242, 1992
A;Title: TRK-T1 is a novel oncogene formed by the fusion of TPR and TRK genes in human p
A;Reference number: S23741; MUID:92195650; PMID:1532241
A;Accession: S23741
A;Molecule type: mRNA
A;Residues: 1-503 <GRE>
A;Cross-references: EMBL:X62947
C;Comment: This sequence is the chimeric product of a translocation mutation.
C;Genetics:
A;Gene: TPR/TRK
C;Keywords: fusion protein

  Query Match   27.7%; Score 1247.5; DB 4; Length 503;
  Best Local Similarity 70.9%; Pred. No. 2.1e-52;
  Matches 234; Conservative   35; Mismatches   38; Indels   23; Gaps   3;

```
Qy         510 VIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLV 569
               :|||||||          |  | |||||||||| ||||||||||||||:|| | :|||||
Db         197 IIENPQYF--------SDACVHHIKRRDIVLKWELGEGAFGKVFLAECHNLLPEQDKMLV 248

Qy         570 AVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFL 629
               ||||||: : :||:|||||||||| |||:|||:|:||| :|  ||:|||||:||||:||
Db         249 AVKALKEASESARQDFQREAELLTMLQHQHIVRFFGVCTEGRPLLMVFEYMRHGDLNRFL 308

Qy         630 RAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGA 689
               |:||||| :|  |:   | | ||| |:| :|||:|:|||||  ||||||||||||||||
Db         309 RSHGPDAKLLAGGED-VAPGPLGLGQLLAVASQVAAGMVYLAGLHFVHRDLATRNCLVGQ 367

Qy         690 NLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTT 749
               |:|||||||||:|||||||               ||| ||||||||||||:||||||
Db         368 GLVVKIGDFGMSRDIYSTDYYR-------------VGGRTMLPIRWMPPESILYRKFTT 413

Qy         750 ESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQR 809
               |||||||||:|||||||||||:|||||| |:|||||| ||||| || ||| :| |||||
Db         414 ESDVWSFGVVLWEIFTYGKQPWYQLSNTEAIDCITQGRELERPRACPPEVYAIMRGCWQR 473

Qy         810 EPQQRLNIKEIYKILHALGKATPIYLDILG 839
               ||||| :||:::  | || :| |:|||:|| 
Db         474 EPQQRHSIKDVHARLQALAQAPPVYLDVLG 503
```

RESULT 15
I51236
brain-derived neurotrophic factor receptor precursor - clawed frog (fragment)
N;Alternate names: receptor tyrosine kinase trkB
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Xenopus sp. (clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C;Accession: I51236
R;Cohen-Cory, S.; Fraser, S.E.
Neuron 12, 747-761, 1994
A;Title: BDNF in the development of the visual system of Xenopus.
A;Reference number: I51236; MUID:94213743; PMID:8068082
A;Accession: I51236
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-282 <COH>
A;Cross-references: GB:S69713; NID:g546784; PIDN:AAB30791.1; PID:g546785
C;Genetics:
A;Gene: trkB
C;Function:
A;Description: regulation of nervous system development; receptor for brain-derived neur
C;Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopr
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; phosphoprote
F;25-282/Domain: protein kinase homology (fragment) <KIN>
F;33-41/Region: protein kinase ATP-binding motif
F;61/Active site: Lys #status predicted
F;196/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

  Query Match   27.0%; Score 1216; DB 2; Length 282;
  Best Local Similarity 77.4%; Pred. No. 3.5e-51;
  Matches 233; Conservative   20; Mismatches   28; Indels   20; Gaps   4;

```
Qy         511 IENPQYFRQG-HNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLV 569
               |||||||  |  | |  ||:|||||| :|||||||||||||||||||||    :||:||
Db           1 IENPQYF--GITNSHLKDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLYREQDKILV  58

Qy         570 AVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFL 629
               ||| ||| :  |||||  |||||||||||:|||||||| :|||||||||||||||||||
Db          59 AVKTLKDASDNARKDFHREAELLTNLQHENIVKFYGVCVEGDPLIMVFEYMKHGDLNKFL 118

Qy         630 RAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGA 689
               |||||||::: :|     ||  |||:||: |||:|||||||||||||| |||||||
Db         119 RAHGPDAVLMAEG---NLLIELTQSQMIHISQQIAAGMVYLASQHFVHRDLPTRNCLVGE 175

Qy         690 NLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTT 749
               |||||||||||||||||||||              |||||||||||||||||||:|||
Db         176 NLLVKIGDFGMSRDVYSTDYYR-------------VGGHTMLPIRWMPPESIMYRRFTT 221
```

```
Qy        750 ESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQR 809
              |||||| ||:|||||||||||:|||| ||||||||||||:||| ||||:||:| |||||
Db        222 ESDVWSLGVVLWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPKEIYDLMRGCWQR 281

Qy        810 E 810
              |
Db        282 E 282
```

Search completed: July 12, 2004, 13:39:29
Job time : 29 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:20:20 ; Search time 18 Seconds
(without alignments)
2427.048 Million cell updates/sec

Title: US-09-966-147-6
Perfect score: 4497
Sequence: 1 MDVSLCPAKCSFWRIFLLGS.....IYKILHALGKATPIYLDILG 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4497	100.0	839	1	TRKC_HUMAN	Q16288 homo sapien
2	4358.5	96.9	864	1	TRKC_RAT	Q03351 rattus norv
3	4193	93.2	825	1	TRKC_PIG	P24786 sus scrofa
4	3997	88.9	827	1	TRKC_CHICK	Q91044 gallus gall
5	2321	51.6	818	1	TRKB_CHICK	Q91987 gallus gall
6	2287.5	50.9	821	1	TRKB_MOUSE	P15209 mus musculu
7	2287.5	50.9	821	1	TRKB_RAT	Q63604 rattus norv
8	2277	50.6	822	1	TRKB_HUMAN	Q16620 homo sapien
9	1973.5	43.9	778	1	TRKA_CHICK	Q91009 gallus gall
10	1961	43.6	796	1	TRKA_HUMAN	P04629 homo sapien
11	1913	42.5	799	1	TRKA_RAT	P35739 rattus norv
12	1150.5	25.6	794	1	TRK1_LYMST	O76997 lymnaea sta
13	700	15.6	685	1	ROR1_DROME	Q24488 drosophila
14	670.5	14.9	724	1	ROR2_DROME	Q9v6k3 drosophila
15	666	14.8	943	1	ROR2_HUMAN	Q01974 homo sapien
16	653.5	14.5	855	1	DDR2_HUMAN	Q16832 homo sapien
17	653	14.5	937	1	ROR1_HUMAN	Q01973 homo sapien
18	652	14.5	944	1	ROR2_MOUSE	Q9z138 mus musculu
19	651.5	14.5	854	1	DDR2_MOUSE	Q62371 mus musculu
20	651.5	14.5	1363	1	ILPR_BRALA	O02466 branchiosto
21	647	14.4	937	1	ROR1_MOUSE	Q9z139 mus musculu
22	635.5	14.1	1300	1	IRR_MOUSE	Q9wtl4 mus musculu
23	633.5	14.1	909	1	DDR1_PANTR	Q7yr43 pan troglod
24	633.5	14.1	913	1	DDR1_HUMAN	Q08345 h epithelia
25	631.5	14.0	1382	1	INSR_HUMAN	P06213 homo sapien
26	629	14.0	910	1	DDR1_RAT	Q63474 rattus norv
27	627.5	14.0	1051	1	PTK7_CHICK	Q91048 gallus gall
28	626.5	13.9	823	1	CEK3_CHICK	P18461 gallus gall
29	620.5	13.8	802	1	FGR4_HUMAN	P22455 homo sapien
30	618.5	13.8	911	1	DDR1_MOUSE	Q03146 mus musculu
31	618.5	13.8	1383	1	INSR_RAT	P15127 rattus norv
32	616.5	13.7	1373	1	IG1R_MOUSE	Q60751 mus musculu
33	615.5	13.7	1372	1	INSR_MOUSE	P15208 mus musculu
34	615	13.7	1370	1	IG1R_RAT	P24062 rattus norv
35	614.5	13.7	819	1	FGR1_CHICK	P21804 gallus gall
36	610	13.6	1367	1	IG1R_HUMAN	P08069 homo sapien
37	609.5	13.6	821	1	FGR2_HUMAN	P21802 homo sapien
38	606.5	13.5	1300	1	IRR_CAVPO	P14617 cavia porce
39	605.5	13.5	640	1	IG1R_BOVIN	Q05688 bos taurus
40	605	13.5	806	1	CEK2_CHICK	P18460 gallus gall
41	604.5	13.4	1070	1	PTK7_HUMAN	Q13308 homo sapien
42	603.5	13.4	821	1	FGR2_MOUSE	P21803 mus musculu
43	602.5	13.4	1297	1	IRR_HUMAN	P14616 homo sapien
44	598.5	13.3	822	1	FGR1_MOUSE	P16092 mus musculu
45	595.5	13.2	1052	1	FGR2_DROME	Q09147 drosophila

ALIGNMENTS

RESULT 1
TRKC_HUMAN
ID TRKC_HUMAN STANDARD; PRT; 839 AA.
AC Q16288; Q12827; Q16289;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NT-3 growth factor receptor precursor (EC 2.7.1.112) (TrkC tyrosine
DE kinase) (GP145-TrkC) (Trk-C).
GN NTRK3 OR TRKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D), AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=95123473; PubMed=7823156;
RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,
RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
RT "Human trks: molecular cloning, tissue distribution, and expression
RT of extracellular domain immunoadhesins.";
RL J. Neurosci. 15:477-491(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A AND C).
RC TISSUE=Fetal brain;
RX MEDLINE=95104834; PubMed=7806211;
RA McGregor L.M., Baylin S.B., Griffin C.A., Hawkins A.L., Nelkin B.D.;
RT "Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal
RT assignment, and evidence for a splice variant.";
RL Genomics 22:267-272(1994).
CC -!- FUNCTION: Receptor for neurotrophin-3 (NT-3). This is a tyrosine-
CC protein kinase receptor. Known substrates for the trk receptors
CC are SHC, PI-3 kinase, and PLCG1. The different isoforms do not
CC have identical signaling properties.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist;
CC Name=A;
CC IsoId=Q16288-1; Sequence=Displayed;
CC Name=B;
CC IsoId=Q16288-2; Sequence=VSP_002925, VSP_002926;
CC Name=C;
CC IsoId=Q16288-3; Sequence=VSP_002927;
CC Name=D;
CC IsoId=Q16288-4; Sequence=VSP_002924;
CC -!- TISSUE SPECIFICITY: Widely expressed, mainly in the nervous
CC tissue. The isoform B is expressed in a relatively large amount in
CC the adult brain comparatively to fetal brain.
CC -!- PTM: Ligand-mediated auto-phosphorylation.
CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin

```
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; S76475; AAB33111.1; -.
DR   EMBL; S76476; AAB33112.1; -.
DR   EMBL; U05012; AAA75374.1; -.
DR   PIR; I73632; I73632.
DR   PIR; I73633; I73633.
DR   PDB; 1WWC; 07-JUL-99.
DR   Genew; HGNC:8033; NTRK3.
DR   MIM; 191316; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005016; F:neurotrophin TRKC receptor activity; TAS.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW   Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW   Leucine-rich repeat; Repeat; Alternative splicing;
KW   Immunoglobulin domain; 3D-structure.
FT   SIGNAL       1     31
FT   CHAIN       32    839       NT-3 GROWTH FACTOR RECEPTOR.
FT   DOMAIN      32    429       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   430    453       POTENTIAL.
FT   DOMAIN     454    839       CYTOPLASMIC (POTENTIAL).
FT   REPEAT     102    125       LRR 1.
FT   REPEAT     126    149       LRR 2.
FT   DOMAIN     210    300       IG-LIKE C2-TYPE 1.
FT   DOMAIN     309    382       IG-LIKE C2-TYPE 2.
FT   DOMAIN     538    839       PROTEIN KINASE.
FT   NP_BIND    544    552       ATP (BY SIMILARITY).
FT   BINDING    572    572       ATP (BY SIMILARITY).
FT   ACT_SITE   679    679       BY SIMILARITY.
FT   MOD_RES    516    516       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES    705    705       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES    709    709       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES    710    710       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES    834    834       PHOSPHORYLATION (BY SIMILARITY).
FT   SITE       516    516       INTERACTION WITH SHC PROTEIN
FT                               (BY SIMILARITY).
FT   SITE       834    834       INTERACTION WITH PLC-GAMMA-1
FT                               (BY SIMILARITY).
FT   CARBOHYD    72     72       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   133    133       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   203    203       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   218    218       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   232    232       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   259    259       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   267    267       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   272    272       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   294    294       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   375    375       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   388    388       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC   402    410       Missing (in isoform D).
FT                               /FTId=VSP_002924.
FT   VARSPLIC   529    612       YVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLV
FT                               AVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDG
FT                               DP -> WVFSNIDNHGILNLKDNRDHLVPSTHYIYEEPEVQ
FT                               SGEVSYPRSHGFREIMLNPISLPGHSKPLNHGIYVEDVNVY
FT                               FSKGRHGF (in isoform B).
FT                               /FTId=VSP_002925.
FT   VARSPLIC   613    839       Missing (in isoform B).
FT                               /FTId=VSP_002926.
FT   VARSPLIC   712    725       Missing (in isoform C).
FT                               /FTId=VSP_002927.
FT   CONFLICT    70     70       N -> S (IN REF. 2).
FT   CONFLICT   635    635       D -> N (IN REF. 2).
SQ   SEQUENCE   839 AA;  94455 MW;  86D965A5003B4DDD CRC64;

  Query Match           100.0%;  Score 4497;  DB 1;  Length 839;
  Best Local Similarity  100.0%;  Pred. No. 5e-269;
  Matches  839;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
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Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839


RESULT 2
TRKC_RAT
ID   TRKC_RAT       STANDARD;      PRT;   864 AA.
AC   Q03351;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   NT-3 growth factor receptor precursor (EC 2.7.1.112) (TrkC tyrosine
DE   kinase) (GP145-TrkC) (Trk-C).
GN   NTRK3 OR TRKC.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM TRKC).
RX   MEDLINE=93140932; PubMed=1488112;
RA   Merlio J.P., Ernfors P., Jaber M., Persson H.;
RT   "Molecular cloning of rat trkC and distribution of cells expressing
RT   messenger RNAs for members of the trk family in the rat central
RT   nervous system.";
RL   Neuroscience 51:513-532(1992).
RN   [2]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=93264091; PubMed=8494647;
RA   Valenzuela D.M., Maisonpierre P.C., Glass D.J., Rojas E., Nunez L.,
RA   Kong Y., Gies D.R., Stitt T.N., Ip N.Y., Yancopoulos G.D.;
RT   "Alternative forms of rat TrkC with different functional
RT   capabilities.";
RL   Neuron 10:963-974(1993).
RN   [3]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Brain cortex, and Hippocampus;
RX   MEDLINE=93264092; PubMed=8494648;
RA   Tsoulfas P., Soppet D., Escandon E., Tessarollo L.,
RA   Mendoza-Ramirez J.-L., Rosenthal A., Nikolics K., Parada L.F.;
RT   "The rat trkC locus encodes multiple neurogenic receptors that
RT   exhibit differential response to neurotrophin-3 in PC12 cells.";
RL   Neuron 10:975-990(1993).
CC   -!- FUNCTION: Receptor for neurotrophin-3 (NTF3). This is a tyrosine-
CC       protein kinase receptor. Known substrates for the TRK receptors
CC       are SHC, PI-3 kinase, and PLCG1. TrkC isoforms containing
CC       insertions within the kinase domain can autophosphorylate in
CC       response to NT-3, but cannot mediate downstream phenotypic
CC       responses.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC       AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=8;
CC         Comment=Additional isoforms seem to exist;
CC       Name=KI39; Synonyms=TRKC(KI39), TRKC-39;
CC         IsoId=Q03351-1; Sequence=Displayed;
CC       Name=TRKC;
CC         IsoId=Q03351-2; Sequence=VSP_002936, VSP_002937;
CC       Name=KI14; Synonyms=TRKC(KI14), TRKC-14;
CC         IsoId=Q03351-3; Sequence=VSP_002936;
CC       Name=KI25; Synonyms=TRKC-25;
CC         IsoId=Q03351-4; Sequence=VSP_002937;
CC       Name=IC158; Synonyms=TRKC(IC158), TRKCTK-;
CC         IsoId=Q03351-5; Sequence=VSP_002934, VSP_002935;
CC       Name=IC143; Synonyms=TRKC(IC143);
CC         IsoId=Q03351-6; Sequence=VSP_002932, VSP_002933;
CC       Name=IC113; Synonyms=TRKC(IC113);
CC         IsoId=Q03351-7; Sequence=VSP_002930, VSP_002931;
CC       Name=IC108; Synonyms=TRKC(IC108);
CC         IsoId=Q03351-8; Sequence=VSP_002928, VSP_002929;
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, MAINLY IN THE NERVOUS
CC       TISSUE.
CC   -!- PTM: Ligand-mediated auto-phosphorylation.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L03813; AAA42285.1; -.
DR   EMBL; L14445; AAA42282.1; -.
DR   EMBL; L14446; AAA42283.1; -.
DR   EMBL; L14447; AAA42284.1; -.
DR   EMBL; S60953; AAB26714.2; -.
DR   EMBL; S62924; AAB26716.2; -.
DR   EMBL; S62933; AAB26715.2; -.
DR   HSSP; P06213; 1IRK.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW   Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW   Leucine-rich repeat; Repeat; Immunoglobulin domain;
KW   Alternative splicing.
FT   SIGNAL        1     31       BY SIMILARITY.
FT   CHAIN        32    864       NT-3 GROWTH FACTOR RECEPTOR.
FT   DOMAIN       32    429       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    430    453       POTENTIAL.
FT   DOMAIN      454    864       CYTOPLASMIC (POTENTIAL).
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FT   REPEAT      102    125       LRR 1.
FT   REPEAT      126    149       LRR 2.
FT   DOMAIN      210    300       IG-LIKE C2-TYPE 1.
FT   DOMAIN      309    382       IG-LIKE C2-TYPE 2.
FT   DOMAIN      538    853       PROTEIN KINASE.
FT   NP_BIND     544    552       ATP (BY SIMILARITY).
FT   BINDING     572    572       ATP (BY SIMILARITY).
FT   ACT_SITE    679    679       BY SIMILARITY.
FT   MOD_RES     516    516       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     705    705       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     709    709       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     710    710       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     859    859       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   SITE        516    516       INTERACTION WITH SHC PROTEIN
FT                                (BY SIMILARITY).
FT   SITE        859    859       INTERACTION WITH PLC-GAMMA-1
FT                                (BY SIMILARITY).
FT   CARBOHYD     68     68       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     72     72       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    133    133       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    203    203       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    218    218       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    232    232       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    259    259       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    267    267       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    272    272       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    294    294       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    375    375       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    388    388       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    529    562       YVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSP -> FGR
FT                                IEGFAYGKRYVVMTSVHCHPCWFRFGGLEWL (in
FT                                isoform IC108).
FT                                /FTId=VSP_002928.
FT   VARSPLIC    563    864       Missing (in isoform IC108).
FT                                /FTId=VSP_002929.
FT   VARSPLIC    529    567       YVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKM
FT                                -> CFREIMLNPISLSGHSKPLNHGIYVEDVNVYFSKGRHG
FT                                F (in isoform IC113).
FT                                /FTId=VSP_002930.
FT   VARSPLIC    568    864       Missing (in isoform IC113).
FT                                /FTId=VSP_002931.
FT   VARSPLIC    529    597       YVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLV
FT                                AVKALKDPTLAARKDFQREAELLTNLQH -> WVFSNIDNH
FT                                GILNLKDNRDHLVPSTHYIYEEPEVQSGDVSYPRSHGELLP
FT                                LTSLYEVKPLPLPVLILKT (in isoform IC143).
FT                                /FTId=VSP_002932.
FT   VARSPLIC    598    864       Missing (in isoform IC143).
FT                                /FTId=VSP_002933.
FT   VARSPLIC    529    612       YVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLV
FT                                AVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDG
FT                                DP -> WVFSNIDNHGILNLKDNRDHLVPSTHYIYEEPEVQ
FT                                SGDVSYPRSHGFREIMLNPISLSGHSKPLNHGIYVEDVNVY
FT                                FSKGRHGF (in isoform IC158).
FT                                /FTId=VSP_002934.
FT   VARSPLIC    613    864       Missing (in isoform IC158).
FT                                /FTId=VSP_002935.
FT   VARSPLIC    712    736       Missing (in isoform KI14 and isoform
FT                                TRKC).
FT                                /FTId=VSP_002936.
FT   VARSPLIC    737    750       Missing (in isoform KI25 and isoform
FT                                TRKC).
FT                                /FTId=VSP_002937.
SQ   SEQUENCE   864 AA;  97063 MW;  A202E993E208F636 CRC64;

  Query Match             96.9%;  Score 4358.5;  DB 1;  Length 864;
  Best Local Similarity   94.3%;  Pred. No. 1.7e-260;
  Matches  815;  Conservative   14;  Mismatches   10;  Indels   25;  Gaps    1;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANININITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:|||||||||||||||||||| |||||||||||||||||||||||:|||
Db         61 DSGNSNGNASININITDISRNITSIHIENWRGLHTLNAVDMELYTGLQKLTIKNSGLRNIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              :|:||:|||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RLDSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              |||||||||| |||:|||||||||||||| |||||:||||||||||::|||||:||
Db        301 VYYPPRVVSLVEPEVRLEHCIEFVVRGNPTPTLHWLYNGQPLRESKIIHMDYYQEGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              |||||||||||||||||||| |||||||||||||||||| |    : |||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNALGTANQTINGHFLKEPFPESTDFFDFESDASPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR--------- 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYREGPYQKGPF 720

Qy        712 ---------------LFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWS 755
                            ||||||||||||||||||||||||||||||||||||||||||||
Db        721 SVSWQQQRLAASAASTLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWS 780

Qy        756 FGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRL 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 FGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRL 840

Qy        816 NIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||
Db        841 NIKEIYKILHALGKATPIYLDILG 864


RESULT 3
TRKC_PIG
ID   TRKC_PIG       STANDARD;      PRT;   825 AA.
AC   P24786;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   NT-3 growth factor receptor precursor (EC 2.7.1.112) (TrkC tyrosine
DE   kinase) (GP145-TrkC) (Trk-C).
GN   NTRK3 OR TRKC.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
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RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=91364178; PubMed=1653651;
RA   Lamballe F., Klein R., Barbacid M.;
RT   "trkC, a new member of the trk family of tyrosine protein kinases, is
RT   a receptor for neurotrophin-3.";
RL   Cell 66:967-979(1991).
CC   -!- FUNCTION: RECEPTOR FOR NEUROTROPHIN-3 (NT-3). THIS IS A TYROSINE-
CC       PROTEIN KINASE RECEPTOR. KNOWN SUBSTRATES FOR THE TRK RECEPTORS
CC       ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC       AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: PREFERENTIALLY IN THE BRAIN, LOW LEVELS IN THE
CC       OVARIES.
CC   -!- PTM: Ligand-mediated auto-phosphorylation.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M80800; AAA31130.1; -.
DR   PIR; A40026; A40026.
DR   HSSP; P06213; 1IRK.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW   Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW   Leucine-rich repeat; Repeat; Immunoglobulin domain.
FT   SIGNAL       1    31       BY SIMILARITY.
FT   CHAIN       32   825       NT-3 GROWTH FACTOR RECEPTOR.
FT   DOMAIN      32   429       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   430   453       POTENTIAL.
FT   DOMAIN     454   825       CYTOPLASMIC (POTENTIAL).
FT   REPEAT     102   125       LRR 1.
FT   REPEAT     126   149       LRR 2.
FT   DOMAIN     210   300       IG-LIKE C2-TYPE 1.
FT   DOMAIN     309   382       IG-LIKE C2-TYPE 2.
FT   DOMAIN     538   814       PROTEIN KINASE.
FT   NP_BIND    544   552       ATP (BY SIMILARITY).
FT   BINDING    572   572       ATP (BY SIMILARITY).
FT   ACT_SITE   679   679       BY SIMILARITY.
FT   MOD_RES    516   516       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES    705   705       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES    709   709       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES    710   710       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES    820   820       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   SITE       516   516       INTERACTION WITH SHC PROTEIN (BY
FT                              SIMILARITY).
FT   SITE       820   820       INTERACTION WITH PLC-GAMMA-1 (BY
FT                              SIMILARITY).
FT   CARBOHYD    68    68       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    72    72       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    79    79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   133   133       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   163   163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   203   203       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   218   218       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   232   232       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   259   259       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   267   267       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   272   272       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   294   294       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   375   375       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   388   388       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   825 AA;  93129 MW;  A3C6716B10D28540 CRC64;

  Query Match             93.2%;  Score 4193;  DB 1;  Length 825;
  Best Local Similarity   94.2%;  Pred. No. 2.4e-250;
  Matches  792;  Conservative   11;  Mismatches   20;  Indels   18;  Gaps    3;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              ||||||||:|||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRGLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              |||||:||||:||||||||||||||||||||||||||||||||||||:||||||||||||
Db        181 KLNSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVVTCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              |:||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db        301 VHYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKITHVEYYQEGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              |||||||||||||||||  : |||||||||||||||||||||: | |||||||||
Db        361 GCLLFNKPTHYNNGNYTLNRQEPLGTANQTINGHFLKEPFPESTDNFVSFYEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHIN--HGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538
              |||    |  |  :   ||    ||||||||||||||||||||||||||||||||||||
Db        481 LHHDQPWHHHTLITGRRAGHS--VIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538

Qy        539 VLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        539 VLKRELGEGAFGKVFLAECYNLSPTKVKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598

Qy        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658

Qy        659 IASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGN 718
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 IASQICSGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR------- 711

Qy        719 DFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 778
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 -------VGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 764

Qy        779 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 838
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 824

Qy        839 G 839
              |
Db        825 G 825
```

RESULT 4
TRKC_CHICK
ID   TRKC_CHICK   STANDARD;   PRT;   827 AA.
AC   Q91044; Q91011; Q92022;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   NT-3 growth factor receptor precursor (EC 2.7.1.112) (TrkC tyrosine
DE   kinase) (Trk-C).
GN   TRKC.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS ALPHA-FL; ALPHA-KT; ALPHA-KD; BETA-KD AND
RP   KI25).
RC   TISSUE=Embryonic brain;
RX   MEDLINE=94338700; PubMed=8060621;
RA   Garner A.S., Large T.H.;
RT   "Isoforms of the avian TrkC receptor: a novel kinase insertion
RT   dissociates transformation and process outgrowth from survival.";
RL   Neuron 13:457-472(1994).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS ALPHA/FL AND TRKC-3).
RX   MEDLINE=93359043; PubMed=8394830;
RA   Okazawa H., Kamei M., Kanazawa I.;
RT   "Molecular cloning and expression of a novel truncated form of
RT   chicken trkC.";
RL   FEBS Lett. 329:171-177(1993).
RN   [3]
RP   SEQUENCE OF 378-513 FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=94084905; PubMed=8261614;
RA   Williams R., Backstrom A., Ebendal T., Hallbook F.;
RT   "Molecular cloning and cellular localization of trkC in the chicken
RT   embryo.";
RL   Brain Res. Dev. Brain Res. 75:235-252(1993).
CC   -!- FUNCTION: Receptor for neurotrophin-3 (NT-3). This is a tyrosine-
CC   protein kinase receptor. Known substrates for the trk receptors
CC   are SHC, PI-3 kinase and PLCG1. The KT and KD isoforms fail to
CC   stimulate transformation, process outgrowth or survival. Isoform
CC   KI25 exhibits tyrosine phosphorylation in the absence of ligand
CC   and is unable to mediate survival of neuronal cells.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC   tyrosine phosphate.
CC   -!- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC   AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=6;
CC   Comment=Additional isoforms seem to exist;
CC   Name=Alpha-FL;
CC   IsoId=Q91044-1; Sequence=Displayed;
CC   Name=Alpha-KT;
CC   IsoId=Q91044-2; Sequence=VSP_002943, VSP_002944;
CC   Name=Alpha-KD;
CC   IsoId=Q91044-3; Sequence=VSP_002939, VSP_002940;
CC   Name=Beta-KD;
CC   IsoId=Q91044-4; Sequence=VSP_002938, VSP_002939, VSP_002940;
CC   Name=TRKC-3;
CC   IsoId=Q91044-5; Sequence=VSP_002941, VSP_002942;
CC   Name=KI25;
CC   IsoId=Q91044-6; Sequence=VSP_002945;
CC   -!- DEVELOPMENTAL STAGE: EXPRESSION OCCURS IN THE EMBRYONAL DAY 2 (E2)
CC   EMBRYO WITH INCREASING LEVELS LATER IN DEVELOPMENT. IN THE E9
CC   EMBRYO HIGHEST LEVELS ARE FOUND IN BRAIN AND SPINAL CORD WITH
CC   INTERMEDIATE LEVELS IN EYE, HEART, GUT AND MUSCLE. LOW LEVELS ARE
CC   FOUND IN KIDNEY, LIVER, SKIN AND YOLK SAC.
CC   -!- PTM: Ligand-mediated auto-phosphorylation (By similarity).
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC   receptor subfamily.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC   -!- CAUTION: THE ADDITIONAL KINASE-DELETED ISOFORM TRKC-3 WHICH
CC   REPLACES THE KINASE DOMAIN WITH 19 AA INSTEAD OF 39 IN THE ISOFORM
CC   ALPHA-KD RESULTS FROM A FRAMESHIFT.
CC   ---
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CC   ---
DR   EMBL; S74248; AAB31699.1; -.
DR   EMBL; X59669; CAA42202.1; -.
DR   EMBL; Z30091; CAA82907.1; -.
DR   PIR; I51222; I51222.
DR   PIR; I51259; I51259.
DR   PIR; S35695; S35695.
DR   HSSP; P06213; 1IRK.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW   Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW   Leucine-rich repeat; Repeat; Alternative splicing;
KW   Immunoglobulin domain.
FT   SIGNAL   1   31   BY SIMILARITY.
FT   CHAIN   32   827   NT-3 GROWTH FACTOR RECEPTOR.
FT   DOMAIN   32   430   EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   431   455   POTENTIAL.
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FT   DOMAIN       456    827       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       102    125       LRR 1.
FT   REPEAT       126    149       LRR 2.
FT   DOMAIN       210    300       IG-LIKE C2-TYPE 1.
FT   DOMAIN       319    382       IG-LIKE C2-TYPE 2.
FT   DOMAIN       540    812       PROTEIN KINASE.
FT   NP_BIND      546    554       ATP (BY SIMILARITY).
FT   BINDING      574    574       ATP (BY SIMILARITY).
FT   ACT_SITE     681    681       BY SIMILARITY.
FT   MOD_RES      518    518       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES      707    707       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES      711    711       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES      712    712       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES      822    822       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   SITE         518    518       INTERACTION WITH SHC PROTEIN
FT                                  (BY SIMILARITY).
FT   SITE         822    822       INTERACTION WITH PLC-GAMMA-1
FT                                  (BY SIMILARITY).
FT   CARBOHYD      68     68       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      72     72       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     203    203       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     218    218       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     232    232       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     259    259       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     267    267       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     272    272       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     294    294       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     375    375       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     388    388       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC       1     98       Missing (in isoform Beta-KD).
FT                                  /FTId=VSP_002938.
FT   VARSPLIC     581    619       LAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVF
FT                                  -> CFREIMLNPISLPGHSKPLNQGIYVEDVSVYFSKGRHG
FT                                  F (in isoform Alpha-KD and isoform
FT                                  Beta-KD).
FT                                  /FTId=VSP_002939.
FT   VARSPLIC     620    827       Missing (in isoform Alpha-KD and isoform
FT                                  Beta-KD).
FT                                  /FTId=VSP_002940.
FT   VARSPLIC     581    599       LAARKDFQREAELLTNLQH -> CFREIMLNPISLPGHCQT
FT                                  S (in isoform TRKC-3).
FT                                  /FTId=VSP_002941.
FT   VARSPLIC     600    827       Missing (in isoform TRKC-3).
FT                                  /FTId=VSP_002942.
FT   VARSPLIC     633    664       AHGPDAMILVDGQPRQAKGELGLSQMLHIASQ -> LEDTP
FT                                  CCLSAGCLRRASCTGSSQRRVTSGASG (in isoform
FT                                  Alpha-KT).
FT                                  /FTId=VSP_002943.
FT   VARSPLIC     665    827       Missing (in isoform Alpha-KT).
FT                                  /FTId=VSP_002944.
FT   VARSPLIC     713    713       R -> REGPRPKGQLSTAWQRHRLAPPAAAT (in
FT                                  isoform KI25).
FT                                  /FTId=VSP_002945.
FT   CONFLICT       1     39       MDVSLCPTKCTFWRVFLLWSIWGDYLLSVLACPANCLCS
FT                                  -> MHFICWRIFASDRLKVLF (IN REF. 2).
FT   CONFLICT     124    124       A -> G (IN REF. 2).
FT   CONFLICT     378    378       I -> F (IN REF. 3).
FT   CONFLICT     481    496       SPLHHINHGITTPSSL -> ATHTSTTDTRFVT (IN
FT                                  REF. 2).
FT   CONFLICT     795    795       W -> C (IN REF. 2).
SQ   SEQUENCE   827 AA;  93180 MW;  AB97373113DCB28A CRC64;

  Query Match             88.9%;  Score 3997;  DB 1;  Length 827;
  Best Local Similarity   88.2%;  Pred. No. 2.7e-238;
  Matches  742;  Conservative   44;  Mismatches   39;  Indels   16;  Gaps    2;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||| ||:|||:||| |:| ||: |||||||||:||||:|||::||||||||||||
Db          1 MDVSLCPTKCTFWRVFLLWSIWGDYLLSVLACPANCLCSKTDINCKKPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||:|||| :|||||||||||||||::| |||||||||||||:|||:|||||:|||
Db         61 DSGSSNGNTSINITDISRNITSIHIENWKNLQTLNAVDMELYTGLQRLTIRNSGLRNIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              |||||||||||:|| |||||||||||||| | :|:||:| |||||||||:|||||:|||
Db        121 RAFAKNPHLRYIDLSGNRLTTLSWQLFQTLRLFDLRLERNPFNCSCDIRWIQLWQEKGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              | || |:|:| | : : |  |||:|||||||||||||||||||:|||||||||||||||
Db        181 NLQSQQLHCMNLDTAVILLRNMNITQCDLPEISVSHVNLTVREGENAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||| |  | |||||||||||||||||||||||||||||||| |||||||||||||||||
Db        241 VDWTVADLHSINTHQTNLNWTNVHAINLTLVNVTSEDNGFLLTCIAENVVGMSNASVLLT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||:::|||| | ||||| | | ||| |||||||||| |||::|||:|:||:|:||
Db        301 VYYPPRILTLEEPVLHLEHCIAFAVHGNPAPTLHWLHNGQVLRETEIIHMEFYQQGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFD--EVSPTPP 418
              |||||||||||||||::| | ||:||||| ||||:|||||||||:      |||||||
Db        361 GCLLFNKPTHYNNGNYTIVATNQLGSANQTIKGHFLEKPFPESTDNFVSIGDYEVSPTPP 420

Qy        419 ITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSA 478
              ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db        421 ITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSA 480

Qy        479 SPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 SPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDI 540

Qy        539 VLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 598
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        541 VLKRELGEGAFGKVFLAECYNLSPTNDKMLVAVKALKDPTLAARKDFQREAELLTNLQHE 600

Qy        599 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 658
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 HIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLH 660

Qy        659 IASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGN 718
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 IASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYR------- 713

Qy        719 DFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 778
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 -------VGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTE 766

Qy        779 VIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 838
              |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db        767 VIECITQGRVLERPRVCPKEVYDIMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDIL 826

Qy        839 G 839
              |
Db        827 G 827


RESULT 5
TRKB_CHICK
ID   TRKB_CHICK     STANDARD;      PRT;   818 AA.
AC   Q91987; Q91010;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   BDNF/NT-3 growth factors receptor precursor (EC 2.7.1.112) (TrkB
DE   tyrosine kinase) (Trk-B).
GN   TRKB.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 10).
```

```
RC   TISSUE=Brain;
RX   MEDLINE=95047511; PubMed=7959025;
RA   Vinh N., Erdmann K., Heumann R.;
RT   "Cloning and sequence analysis of a cDNA encoding a novel truncated
RT   form of the chicken TrkB receptor.";
RL   Gene 149:383-384(1994).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=94116452; PubMed=8287802;
RA   Dechant G., Biffo S., Okazawa H., Kolbeck R., Pottgiesser J.,
RA   Barde Y.-A.;
RT   "Expression and binding characteristics of the BDNF receptor chick
RT   trkB.";
RL   Development 119:545-558(1993).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE FROM N.A.
RP   (ISOFORMS 2; 3; 4; 5; 6; 7; 8; 9; 10; 11 AND 12).
RX   MEDLINE=96370546; PubMed=8774442;
RA   Garner A.S., Menegay H.J., Boeshore K.L., Xie X.Y., Voci J.M.,
RA   Johnson J.E., Large T.H.;
RT   "Expression of TrkB receptor isoforms in the developing avian visual
RT   system.";
RL   J. Neurosci. 16:1740-1752(1996).
CC   -!- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
CC       NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
CC       (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
CC       NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
CC       SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
CC       GAMMA-1 (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC       AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=12;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1; Synonyms=Alpha-FL;
CC         IsoId=Q91987-1; Sequence=Displayed;
CC       Name=2; Synonyms=Beta-FL;
CC         IsoId=Q91987-2; Sequence=VSP_002914;
CC       Name=3; Synonyms=ED;
CC         IsoId=Q91987-3; Sequence=VSP_002915;
CC       Name=4; Synonyms=JD;
CC         IsoId=Q91987-4; Sequence=VSP_002923;
CC       Name=5; Synonyms=J1;
CC         IsoId=Q91987-5; Sequence=VSP_002920;
CC       Name=6; Synonyms=Alpha-T1;
CC         IsoId=Q91987-6; Sequence=VSP_002918, VSP_002919;
CC       Name=7; Synonyms=J1+T1;
CC         IsoId=Q91987-7; Sequence=VSP_002918, VSP_002919, VSP_002920;
CC       Name=8; Synonyms=J2+T1;
CC         IsoId=Q91987-8; Sequence=VSP_002918, VSP_002919, VSP_002921;
CC       Name=9; Synonyms=ED J2+T1;
CC         IsoId=Q91987-9; Sequence=VSP_002915, VSP_002918, VSP_002919,
CC                                  VSP_002921;
CC       Name=10; Synonyms=J1+J2+T1;
CC         IsoId=Q91987-10; Sequence=VSP_002918, VSP_002919, VSP_002922;
CC       Name=11; Synonyms=T3;
CC         IsoId=Q91987-11; Sequence=VSP_002916, VSP_002917;
CC       Name=12; Synonyms=ED J1+J2+T1;
CC         IsoId=Q91987-12; Sequence=VSP_002915, VSP_002918, VSP_002919,
CC                                  VSP_002922;
CC   -!- PTM: Ligand-mediated auto-phosphorylation.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   -!- CAUTION: IT IS UNCERTAIN WHETHER LEU-144 OR MET-188 IS THE
CC       INITIATOR OF ISOFORM 2.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X77251; CAA54468.1; -.
DR   EMBL; X77252; CAA54469.1; -.
DR   EMBL; X74109; CAA52210.1; -.
DR   PIR; S59939; S44098.
DR   HSSP; P06213; 1IRK.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW   Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW   Leucine-rich repeat; Repeat; Alternative splicing;
KW   Immunoglobulin domain.
FT   SIGNAL        1     31       BY SIMILARITY.
FT   CHAIN        32    818       BDNF/NT-3 GROWTH FACTORS RECEPTOR.
FT   DOMAIN       32    426       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    427    450       POTENTIAL.
FT   DOMAIN      451    818       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       71     92       LRR 1.
FT   REPEAT       95    116       LRR 2.
FT   DOMAIN      196    281       IG-LIKE C2-TYPE 1.
FT   DOMAIN      295    364       IG-LIKE C2-TYPE 2.
FT   DOMAIN      534    803       PROTEIN KINASE.
FT   NP_BIND     540    548       ATP (BY SIMILARITY).
FT   BINDING     568    568       ATP (BY SIMILARITY).
FT   ACT_SITE    672    672       BY SIMILARITY.
FT   DISULFID     32     38       BY SIMILARITY.
FT   DISULFID     36     45       BY SIMILARITY.
FT   DISULFID    151    175       BY SIMILARITY.
FT   DISULFID    153    193       BY SIMILARITY.
FT   DISULFID    217    265       BY SIMILARITY.
FT   DISULFID    301    344       BY SIMILARITY.
FT   MOD_RES     512    512       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     698    698       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     702    702       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     703    703       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     813    813       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   SITE        512    512       INTERACTION WITH SHC PROTEIN
FT                                (BY SIMILARITY).
FT   SITE        813    813       INTERACTION WITH PLC-GAMMA-1
FT                                (BY SIMILARITY).
FT   CARBOHYD     66     66       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     94     94       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    120    120       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    199    199       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    204    204       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    226    226       N-LINKED (GLCNAC. . .) (POTENTIAL).
```

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FT   CARBOHYD    253    253       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    287    287       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    324    324       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    337    337       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    408    408       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1    143       Missing (in isoform 2).
FT                                /FTId=VSP_002914.
FT   VARSPLIC    384    394       Missing (in isoform 3, isoform 9 and
FT                                isoform 12).
FT                                /FTId=VSP_002915.
FT   VARSPLIC    462    467       GPSSVI -> ERGRRK (in isoform 11).
FT                                /FTId=VSP_002916.
FT   VARSPLIC    468    818       Missing (in isoform 11).
FT                                /FTId=VSP_002917.
FT   VARSPLIC    463    473       PSSVISNDDDS -> FVLFHKIPLDG (in isoform 6,
FT                                isoform 7, isoform 8, isoform 9, isoform
FT                                10 and isoform 12).
FT                                /FTId=VSP_002918.
FT   VARSPLIC    474    818       Missing (in isoform 6, isoform 7, isoform
FT                                8, isoform 9, isoform 10 and isoform 12).
FT                                /FTId=VSP_002919.
FT   VARSPLIC    462    462       G -> VHGEVKGVGLVDQIWLSLQDCDNEG (in
FT                                isoform 5 and isoform 7).
FT                                /FTId=VSP_002920.
FT   VARSPLIC    462    462       G -> EQVMVTVNSDVHNNSTASDNNRLG (in isoform
FT                                8 and isoform 9).
FT                                /FTId=VSP_002921.
FT   VARSPLIC    462    462       G -> VHGEVKGVGLVDQIWLSLQDCDNEEQVMVTVNSDVH
FT                                NNSTASDNNRLG (in isoform 10 and isoform
FT                                12).
FT                                /FTId=VSP_002922.
FT   VARSPLIC    462    465       Missing (in isoform 4).
FT                                /FTId=VSP_002923.
SQ   SEQUENCE   818 AA;  91736 MW;  D1BA39E2092B2152 CRC64;

  Query Match             51.6%;  Score 2321;  DB 1;  Length 818;
  Best Local Similarity   53.8%;  Pred. No. 2.8e-135;
  Matches  463;  Conservative  120;  Mismatches  193;  Indels   84;  Gaps   15;

Qy          5 LCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDG-NLFPLLEGQDSG 63
              ||      ||                | |||:| ||    | |  |   |    ||: :
Db         18 LCCLVLGCWR-------------GALGCPASCRCSSWRIWCSEPVPGITSFPVPQRSTED 64

Qy         64 NSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAF 123
              :          |:| |:| | | | ::|  ::  | ||: ||: :|||| :  :||
Db         65 D--------------NVTEIYIANQRKLESINDNEVGFYVGLKNLTVVDSGLRFVSRQAF 110

Qy        124 AKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLN 183
               || :|:|||| |:|::|| : |: | | :| |  | | ||||:| |:: :||  :
Db        111 VKNINLQYINLSRNKLSSLSKKPFRHLGLSDLILVDNPFKCSCEIMWIKKFQET-KFYTE 169

Qy        184 SQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDW 243
              :|::||:: :  :: |  | :  |||| ::|: |:|| ||  :  : |: :| | |:| |
Db        170 AQDIYCVDDNNKRIALMDMKVPNCDLPSANLSNYNITVVEGKSITLYCDTTGGPPPNVSW 229

Qy        244 IVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYY 303
              ::| |  :: |:::   |: :  :||: ||:| |:|  ::|:|||:||    |  |||::
Db        230 VLTNL--VSNHESD---TSKNPASLTIKNVSSMDSGLWISCVAENIVGEVQTSAELTVFF 284

Qy        304 PPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKI----IHV----EYYQE 355
               |  :  :| |       || | |:||| ||| | : | | ||:     |||    ||:
Db        285 APNITFIESPTPDHHWCIPFTVKGNPKPTLQWFYEGAILNESEYICTKIHVINQSEYH-- 342

Qy        356 GEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFP----------E 402
                 |||  : ||| ||| |||:|||  |   : :: ||:  |              |
Db        343 -----GCLQLDNPTHLNNGAYTLLAKNEYGEDEKRVDAHFMSVPGDGSGPIVDPDVYEYE 397

Qy        403 STDNFILFDEVSPTPPIT---VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRR 459
              :| |  | |  : :  ||   |::|  ||:  | : ||:||  |  ||:: ::: |:||
Db        398 TTPN-DLGDTTNNSNQITSPDVSNKENEDSITVYVVVGIAALVCTGLVIMLIIL-KFGRH 455

Qy        460 SKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQ 519
              |||||||| :||| ::|||||||||::|  |||| : ||| |:||||:||||||||||

Db        456 SKFGMKGPSSVISNDDDSASPLHHISNGSNTPSSSEGGPDAVIIGMTKIPVIENPQYFGI 515

Qy        520 GHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTL 579
               ::  ||||:|||||| :|||||||||||||||||||| | :||:||||| ||| :
Db        516 TNSQLKPDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLCPEQDKILVAVKTLKDASD 575

Qy        580 AARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMIL 639
              |||||  |||||||||||||||||||||| :|||||||||||||||||||||||||:::
Db        576 NARKDFHREAELLTNLQHEHIVKFYGVCVEGDPLIMVFEYMKHGDLNKFLRAHGPDAVLM 635

Qy        640 VDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFG 699
               :|       ||  ||||||| |||:|||||||||||||||||||||| ||||||||||
Db        636 AEG---NRPAELTQSQMLHIAQQIAAGMVYLASQHFVHRDLATRNCLVGENLLVKIGDFG 692

Qy        700 MSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVI 759
              ||||||||||||                |||||||||||||||||||||||||||||| ||:
Db        693 MSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTESDVWSLGVV 738

Qy        760 LWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKE 819
              ||||||||||||:|||| ||||||||||||:||| |||||||:|||||||| ||||||
Db        739 LWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPKEVYDLMLGCWQREPHMRLNIKE 798

Qy        820 IYKILHALGKATPIYLDILG 839
              |: :|  | ||:|:||||||
Db        799 IHSLLQNLAKASPVYLDILG 818


RESULT 6
TRKB_MOUSE
ID   TRKB_MOUSE     STANDARD;      PRT;   821 AA.
AC   P15209;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   BDNF/NT-3 growth factors receptor precursor (EC 2.7.1.112) (TrkB
DE   tyrosine kinase) (GP145-TrkB/GP95-TrkB) (Trk-B).
GN   NTRK2 OR TRKB.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM GP145-TRKB).
RC   TISSUE=Brain;
RX   MEDLINE=90059970; PubMed=2555172;
RA   Klein R., Parada L.F., Coulier F., Barbacid M.;
RT   "trkB, a novel tyrosine protein kinase receptor expressed during
RT   mouse neural development.";
RL   EMBO J. 8:3701-3709(1989).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS GP145-TRKB AND GP95-TRKB).
RC   TISSUE=Brain;
RX   MEDLINE=90263089; PubMed=2160854;
RA   Klein R., Conway D., Parada L.F., Barbacid M.;
RT   "The trkB tyrosine protein kinase gene codes for a second neurogenic
RT   receptor that lacks the catalytic kinase domain.";
RL   Cell 61:647-656(1990).
RN   [3]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORMS L1 AND L10).
RC   TISSUE=Trigeminal ganglion;
RX   MEDLINE=97294706; PubMed=9148911;
RA   Ninkina N., Grashchuck M., Buchman V.L., Davies A.M.;
RT   "TrkB variants with deletions in the leucine-rich motifs of the
RT   extracellular domain.";
RL   J. Biol. Chem. 272:13019-13025(1997).
RN   [4]
RP   FUNCTION.
RX   MEDLINE=91249395; PubMed=1645620;
RA   Soppet D., Escandon E., Maragos J., Middlemas D.S., Reid S.W.,
RA   Blair J., Burton L.E., Stanton B.R., Kaplan D.R., Hunter T.,
RA   Nicolics K., Parada L.F.;
RT   "The neurotrophic factors brain-derived neurotrophic factor and
RT   neurotrophin-3 are ligands for the trkB tyrosine kinase receptor.";
```

```
RL   Cell 65:895-903(1991).
CC   -!- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
CC       NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
CC       (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
CC       NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
CC       SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
CC       GAMMA-1.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC       AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC         Comment=Additional isoforms seem to exist;
CC       Name=GP145-TRKB; Synonyms=L3;
CC         IsoId=P15209-1; Sequence=Displayed;
CC       Name=GP95-TRKB; Synonyms=T1;
CC         IsoId=P15209-2; Sequence=VSP_002908, VSP_002909;
CC       Name=L1;
CC         IsoId=P15209-3; Sequence=VSP_002907;
CC       Name=L10;
CC         IsoId=P15209-4; Sequence=VSP_002905, VSP_002906;
CC   -!- TISSUE SPECIFICITY: THE DIFFERENT FORMS ARE DIFFERENTIALLY
CC       EXPRESSED IN VARIOUS CELL TYPES.
CC   -!- PTM: Ligand-mediated auto-phosphorylation.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M33385; AAA40482.1; -.
DR   EMBL; X17647; CAA35636.1; -.
DR   PIR; S06943; S06943.
DR   HSSP; P06213; 1IRK.
DR   MGD; MGI:97384; Ntrk2.
DR   GO; GO:0005829; C:cytosol; IDA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW   Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW   Leucine-rich repeat; Repeat; Immunoglobulin domain;
KW   Alternative splicing.
FT   SIGNAL       1    31
FT   CHAIN       32   821       BDNF/NT-3 GROWTH FACTORS RECEPTOR.
FT   DOMAIN      32   429       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   430   453       POTENTIAL.
FT   DOMAIN     454   821       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      72    93       LRR 1.
FT   REPEAT      96   117       LRR 2.
FT   DOMAIN     197   282       IG-LIKE C2-TYPE 1.
FT   DOMAIN     301   365       IG-LIKE C2-TYPE 2.
FT   DOMAIN     537   806       PROTEIN KINASE.
FT   NP_BIND    543   551       ATP (BY SIMILARITY).
FT   BINDING    571   571       ATP (BY SIMILARITY).
FT   ACT_SITE   675   675       BY SIMILARITY.
FT   DISULFID    32    38       BY SIMILARITY.
FT   DISULFID    36    45       BY SIMILARITY.
FT   DISULFID   152   176       BY SIMILARITY.
FT   DISULFID   154   194       BY SIMILARITY.
FT   DISULFID   218   266       BY SIMILARITY.
FT   DISULFID   302   345       BY SIMILARITY.
FT   MOD_RES    515   515       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES    701   701       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES    705   705       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES    706   706       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES    816   816       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   SITE       515   515       INTERACTION WITH SHC PROTEIN
FT                              (BY SIMILARITY).
FT   SITE       816   816       INTERACTION WITH PLC-GAMMA-1
FT                              (BY SIMILARITY).
FT   CARBOHYD    67    67       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    95    95       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   121   121       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   178   178       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   205   205       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   241   241       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   254   254       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   280   280       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   325   325       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   338   338       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   411   411       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    71    71       I -> M (in isoform L10).
FT                              /FTId=VSP_002905.
FT   VARSPLIC    72   143       Missing (in isoform L10).
FT                              /FTId=VSP_002906.
FT   VARSPLIC    72   120       Missing (in isoform L1).
FT                              /FTId=VSP_002907.
FT   VARSPLIC   466   476       PASVISNDDDS -> FVLFHKIPLDG (in isoform
FT                              GP95-TRKB).
FT                              /FTId=VSP_002908.
FT   VARSPLIC   477   821       Missing (in isoform GP95-TRKB).
FT                              /FTId=VSP_002909.
SQ   SEQUENCE   821 AA;  92133 MW;  50E08D5FF86D8F30 CRC64;

  Query Match             50.9%;  Score 2287.5;  DB 1;  Length 821;
  Best Local Similarity   54.0%;  Pred. No. 3.2e-133;
  Matches  466;  Conservative  110;  Mismatches  206;  Indels   81;  Gaps   15;

Qy          7 PAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDSGNS 65
              ||     | : ||     | :  : |||| :| ||   | |  |  | : || ||
Db         10 PAMARLWGLCLL---VLGFWRASLACPTSCKCSSARIWCTEPSPGIVAFPRLEP------ 60

Qy         66 NGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAK 125
                 |  |   ||| | | | : |  :|  |:| | ||: ||| :|||: :  :|| |
Db         61 ------NSVD-PENITEILIANQKRLEIINEDDVEAYVGLRNLTIVDSGLKFVAYKAFLK 113

Qy        126 NPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQ 185
              | :||:|| : |:||:|| : |: | | :| | | | |||| |::  ||  ::  ::|
Db        114 NSNLRHINFTRNKLTSLSRRHFRHLDLSDLILTGNPFTCSCDIMWLKTLQET-KSSPDTQ 172

Qy        186 NLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIV 245
              :|||:|     :||  : |  | ||   ::  |||| || :  ::|:  | ||| : | |
Db        173 DLYCLNESSKNMPLANLQIPNCGLPSARLAAPNLTVEEGKSVTLSCSVGGDPLPTLYWDV 232
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Qy        246 TGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPP 305
Db        233 GNLVS-----KHMNETSHTQGSLRITNISSDDSGKQISCVAENLVGEDQDSVNLTVHFAP 287

Qy        306 RVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKII--------HVEYYQEGE 357
Db        288 TITFLESPTSDHHWCIPFTVRGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYH---- 343

Qy        358 ISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEP---------FPESTDNFI 408
Db        344 ---GCLQLDNPTHMNNGDYTLMAKNEYGKDERQISAHFMGRPGVDYETNPNYPE-----V 395

Qy        409 LFDE-VSPTPPITVTHK----PEEDTFGVSIAVGLAAFACVLL-------VVLFVMINKY 456
Db        396 LYEDWTTPTDIGDTTNKSNEIPSTDVADQSNREHLSVYAVVVIASVVGFCLLVMLLLLKL 455

Qy        457 GRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQY 516
Db        456 ARHSKFGMKGPASVISNDDDSASPLHHISNGSNTPSSSEGGPDAVIIGMTKIPVIENPQY 515

Qy        517 FRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKD 576
Db        516 FGITNSQLKPDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLCPEQDKILVAVKTLKD 575

Qy        577 PTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDA 636
Db        576 ASDNARKDFHREAELLTNLQHEHIVKFYGVCVEGDPLIMVFEYMKHGDLNKFLRAHGPDA 635

Qy        637 MILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIG 696
Db        636 VLMAEGNP---PTELTQSQMLHIAQQIAAGMVYLASQHFVHRDLATRNCLVGENLLVKIG 692

Qy        697 DFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSF 756
Db        693 DFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTESDVWSL 738

Qy        757 GVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLN 816
Db        739 GVVLWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPQEVYELMLGCWQREPHTRKN 798

Qy        817 IKEIYKILHALGKATPIYLDILG 839
Db        799 IKSIHTLLQNLAKASPVYLDILG 821
```

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RESULT 7
TRKB_RAT
ID   TRKB_RAT       STANDARD;      PRT;   821 AA.
AC   Q63604; Q63605; Q63606;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   BDNF/NT-3 growth factors receptor precursor (EC 2.7.1.112) (TrkB
DE   tyrosine kinase) (GP145-TrkB/GP95-TrkB) (Trk-B).
GN   NTRK2 OR TRKB.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Cerebellum;
RX   MEDLINE=91094826; PubMed=1846020;
RA   Middlemas D.S., Lindberg R.A., Hunter T.;
RT   "trkB, a neural receptor protein-tyrosine kinase: evidence for a
RT   full-length and two truncated receptors.";
RL   Mol. Cell. Biol. 11:143-153(1991).
RN   [2]
RP   PHOSPHORYLATION SITES.
RX   MEDLINE=94149017; PubMed=8106527;
RA   Middlemas D.S., Meisenhelder J., Hunter T.;
RT   "Identification of TrkB autophosphorylation sites and evidence that
RT   phospholipase C-gamma 1 is a substrate of the TrkB receptor.";
RL   J. Biol. Chem. 269:5458-5466(1994).
CC   -!- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
CC       NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
CC       (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
CC       NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
CC       SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
CC       GAMMA-1.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC       AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=GP145-TrkB;
CC         IsoId=Q63604-1; Sequence=Displayed;
CC       Name=T1; Synonyms=GP95-TrkB;
CC         IsoId=Q63604-2; Sequence=VSP_002910, VSP_002911;
CC       Name=T2;
CC         IsoId=Q63604-3; Sequence=VSP_002912, VSP_002913;
CC   -!- TISSUE SPECIFICITY: THE DIFFERENT FORMS ARE DIFFERENTIALLY
CC       EXPRESSED IN VARIOUS CELL TYPES. THE T2 ISOFORM IS PRIMARILY
CC       EXPRESSED IN NEURONS.
CC   -!- PTM: Ligand-mediated auto-phosphorylation.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55291; AAA42279.1; -.
DR   EMBL; M55292; AAA42280.1; -.
DR   EMBL; M55293; AAA42281.1; -.
DR   PIR; A39667; A39667.
DR   PIR; B39667; B39667.
DR   PIR; C39667; C39667.
DR   HSSP; P06213; 1IRK.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW   Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW   Leucine-rich repeat; Repeat; Immunoglobulin domain;
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```
KW   Alternative splicing.
FT   SIGNAL        1     31       BY SIMILARITY.
FT   CHAIN        32    821       BDNF/NT-3 GROWTH FACTORS RECEPTOR.
FT   DOMAIN       32    429       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    430    453       POTENTIAL.
FT   DOMAIN      454    821       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       72     93       LRR 1.
FT   REPEAT       96    117       LRR 2.
FT   DOMAIN      197    282       IG-LIKE C2-TYPE 1.
FT   DOMAIN      295    365       IG-LIKE C2-TYPE 2.
FT   DOMAIN      537    806       PROTEIN KINASE.
FT   NP_BIND     543    551       ATP (BY SIMILARITY).
FT   BINDING     571    571       ATP (BY SIMILARITY).
FT   ACT_SITE    675    675       BY SIMILARITY.
FT   DISULFID     32     38       BY SIMILARITY.
FT   DISULFID     36     45       BY SIMILARITY.
FT   DISULFID    152    176       BY SIMILARITY.
FT   DISULFID    154    194       BY SIMILARITY.
FT   DISULFID    218    266       BY SIMILARITY.
FT   DISULFID    302    345       BY SIMILARITY.
FT   MOD_RES     515    515       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     701    701       PHOSPHORYLATION (AUTO-).
FT   MOD_RES     705    705       PHOSPHORYLATION (AUTO-).
FT   MOD_RES     706    706       PHOSPHORYLATION (AUTO-).
FT   MOD_RES     816    816       PHOSPHORYLATION (AUTO-).
FT   SITE        515    515       INTERACTION WITH SHC PROTEIN
FT                                (BY SIMILARITY).
FT   SITE        816    816       INTERACTION WITH PLC-GAMMA-1
FT                                (BY SIMILARITY).
FT   CARBOHYD     67     67       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    121    121       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    178    178       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    205    205       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    241    241       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    254    254       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    280    280       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    325    325       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    338    338       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    411    411       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    466    476       PASVISNDDDS -> FVLFHKIPLDG (in isoform
FT                                T1).
FT                                /FTId=VSP_002910.
FT   VARSPLIC    477    821       Missing (in isoform T1).
FT                                /FTId=VSP_002911.
FT   VARSPLIC    466    474       PASVISNDD -> KQKCAYFAS (in isoform T2).
FT                                /FTId=VSP_002912.
FT   VARSPLIC    475    821       Missing (in isoform T2).
FT                                /FTId=VSP_002913.
SQ   SEQUENCE   821 AA;  92186 MW;  0DDACDA212CDAA0E CRC64;

  Query Match           50.9%;  Score 2287.5;  DB 1;  Length 821;
  Best Local Similarity   54.0%;  Pred. No. 3.2e-133;
  Matches  468;  Conservative  106;  Mismatches  204;  Indels   89;  Gaps   16;

Qy          7 PAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDSGNS 65
              ||    | : ||    | :  : |||| :| || | | |  |  | : || ||
Db         10 PAMARLWGLCLL---VLGFWRASLACPMSCKCSTTRIWCTEPSPGIVAFPRLEP------ 60

Qy         66 NGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAK 125
                |   ||| | | | : |  :|  :| | ||: ||| :|||: :  :|| |
Db         61 ------NSID-PENITEILIANQKRLEIINEDDVEAYVGLKNLTIVDSGLKFVAYKAFLK 113

Qy        126 NPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQ 185
              | :||:|| : |:||:|| : |: | | :| |  | | ||||| |::  ||  ::  ::|
Db        114 NGNLRHINFTRNKLTSLSRRHFRHLDLSDLILTGNPFTCSCDIMWLKTLQET-KSSPDTQ 172

Qy        186 NLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIV 245
              :|||:|      ||  : |  | ||   ::  |||| || :  |:|:  | ||| : | |
Db        173 DLYCLNESSKNTPLANLQIPNCGLPSARLAAPNLTVEEGKSVTISCSVGGDPLPTLYWDV 232

Qy        246 TGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPP 305
                | |      ::| |:    :| : |::|:|:|  ::|:|||:||    || |||:: |

Db        233 GNLVS-----KHMNETSHTQGSLRITNISSDDSGKQISCVAENLVGEDQDSVNLTVHFAP 287

Qy        306 RVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKII--------HVEYYQEGE 357
              :  || |      || | ||||| | | | :||  | ||| |        | ||:
Db        288 TITFLESPTSDHHWCIPFTVRGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYH---- 343

Qy        358 ISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEP---------FPESTDNFI 408
                |||  : ||| |||:|||:|||  |   : |: ||:  |          :||     :
Db        344 ---GCLQLDNPTHMNNGDYTLMAKNEYGKDERQISAHFMGRPGVDYETNPNYPE-----V 395

Qy        409 LFDE-VSPTPPITVTHKPEE--------------DTFGVSIAVGLAAFACVLLVVLFVM 452
              |::  :||      |:|  |                 : | :   :  | |:|:::| :
Db        396 LYEDWTTPTDIGDTTNKSNEIPSTDVADQTNREHLSVYAVVVIASVVGF-CLLVMLLL- 453

Qy        453 INKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIE 512
                |  | |||||||| :||| ::|||||||||::|  |||| : ||| |:||||:|||||
Db        454 --KLARHSKFGMKGPASVISNDDDSASPLHHISNGSNTPSSSEGGPDAVIIGMTKIPVIE 511

Qy        513 NPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVK 572
              |||||   ::  ||||:|||||| :|||||||||||||||||||| | :||:|||||
Db        512 NPQYFGITNSQLKPDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLCPEQDKILVAVK 571

Qy        573 ALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAH 632
                ||| :  ||||| |||||||||||||||||| :|||||||||||||||||||||||||
Db        572 TLKDASDNARKDFHREAELLTNLQHEHIVKFYGVCVEGDPLIMVFEYMKHGDLNKFLRAH 631

Qy        633 GPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLL 692
              ||||::: :| |      ||  ||||||| |||:|||||||||||||||||||||| |||
Db        632 GPDAVLMAEGNP---PTELTQSQMLHIAQQIAAGMVYLASQHFVHRDLATRNCLVGENLL 688

Qy        693 VKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESD 752
              ||||||||||||||||||                  ||||||||||||||||||||||||
Db        689 VKIGDFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRKFTTESD 734

Qy        753 VWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQ 812
              ||| ||:|||||||||||:|||| ||||||||||:||| ||:|||::|||||||||
Db        735 VWSLGVVLWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPQEVYELMLGCWQREPH 794

Qy        813 QRLNIKEIYKILHALGKATPIYLDILG 839
              | ||| |: :|  | ||:|:||||||
Db        795 TRKNIKNIHTLLQNLAKASPVYLDILG 821


RESULT 8
TRKB_HUMAN
ID   TRKB_HUMAN     STANDARD;      PRT;   822 AA.
AC   Q16620; Q16675;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   BDNF/NT-3 growth factors receptor precursor (EC 2.7.1.112) (TrkB
DE   tyrosine kinase) (GP145-TrkB) (Trk-B).
GN   NTRK2 OR TRKB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM TRKB).
RC   TISSUE=Hippocampus;
RX   MEDLINE=95309922; PubMed=7789988;
RA   Nakagawara A., Liu X.-G., Ikegaki N., White P.S., Yamashiro D.J.,
RA   Nycum L.M., Biegel J.A., Brodeur G.M.;
RT   "Cloning and chromosomal localization of the human TRK-B tyrosine
RT   kinase receptor gene (NTRK2).";
RL   Genomics 25:538-546(1995).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS TRKB AND TRKB-T1).
RC   TISSUE=Brain;
RX   MEDLINE=95123473; PubMed=7823156;
RA   Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,
RA   Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
RT   "Human trks: molecular cloning, tissue distribution, and expression
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RT   of extracellular domain immunoadhesins.";
RL   J. Neurosci. 15:477-491(1995).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM TRKB-T1).
RC   TISSUE=Hippocampus;
RX   MEDLINE=95022162; PubMed=7936202;
RA   Allen S.J., Dawbarn D., Eckford S.D., Wilcock G.K., Ashcroft M.,
RA   Colebrook S.M., Feeney R., Macgowan S.H.;
RT   "Cloning of a non-catalytic form of human trkB and distribution of
RT   messenger RNA for trkB in human brain.";
RL   Neuroscience 60:825-834(1994).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS TRKB; TRKB-T1 AND TRKB-T-SHC).
RX   MEDLINE=21656983; PubMed=11798182;
RA   Stoilov P., Castren E., Stamm S.;
RT   "Analysis of the human TrkB gene genomic organization reveals novel
RT   TrkB isoforms, unusual gene length, and splicing mechanism.";
RL   Biochem. Biophys. Res. Commun. 290:1054-1065(2002).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM TRKB-T1), AND VARIANT ARG-309.
RA   Steinbeck J.A., Thomsen S., Wessig J., Leypoldt F., Lewerenz J.,
RA   Methner A.;
RT   "Full length truncated TrkB sequence identified in a screen for genes
RT   regulated by ischemic preconditioning.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM TRKB-T1).
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   DISULFIDE BONDS.
RX   MEDLINE=96004804; PubMed=7574684;
RA   Haniu M., Talvenheimo J., Le J., Katta V., Welcher A., Rohde M.F.;
RT   "Extracellular domain of neurotrophin receptor trkB: disulfide
RT   structure, N-glycosylation sites, and ligand binding.";
RL   Arch. Biochem. Biophys. 322:256-264(1995).
CC   -!- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
CC       NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
CC       (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
CC       NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
CC       SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
CC       GAMMA-1.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC       AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=TrkB;
CC         IsoId=Q16620-1; Sequence=Displayed;
CC       Name=TrkB-T1;
CC         IsoId=Q16620-2; Sequence=VSP_002901, VSP_002902;
CC       Name=TrkB-T-Shc;
CC         IsoId=Q16620-3; Sequence=VSP_002903, VSP_002904;
CC   -!- TISSUE SPECIFICITY: Isoform TrkB is widely expressed, mainly in
CC       the nervous tissue. In the CNS, expression is observed in the
CC       cerebral cortex, hippocampus, thalamus, choroid plexus, granular
CC       layer of the cerebellum, brain stem, and spinal cord. In the
CC       peripheral nervous system, it is expressed in many cranial
CC       ganglia, the ophtalmic nerve, the vestibular system, multiple
CC       facial structures, the submaxillary glands, and dorsal root
CC       ganglia. Isoform TrkB-T1 is expressed in multiple tissues, mainly
CC       in brain, pancreas, kidney and heart. Isoform TrkB-T-Shc is
CC       predominantly expressed in brain.
CC   -!- PTM: Ligand-mediated auto-phosphorylation.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U12140; AAC51371.1; -.
DR   EMBL; S76473; AAB33109.1; -.
DR   EMBL; S76474; AAB33110.1; -.
DR   EMBL; X75958; CAA53571.1; -.
DR   EMBL; AF410900; -; NOT_ANNOTATED_CDS.
DR   EMBL; AF508964; AAM77876.1; -.
DR   EMBL; BC031835; AAH31835.1; -.
DR   PIR; A56853; A56853.
DR   PIR; I73631; I73631.
DR   PDB; 1HCF; 06-DEC-01.
DR   PDB; 1WWB; 17-AUG-99.
DR   Genew; HGNC:8032; NTRK2.
DR   MIM; 600456; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005015; F:neurotrophin TRKB receptor activity; TAS.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW   Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
KW   Leucine-rich repeat; Repeat; Immunoglobulin domain;
KW   Alternative splicing; Polymorphism; 3D-structure.
FT   SIGNAL       1     31
```

```
FT   CHAIN        32    822       BDNF/NT-3 GROWTH FACTORS RECEPTOR.
FT   DOMAIN       32    430       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    431    454       POTENTIAL.
FT   DOMAIN      455    822       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       72     93       LRR 1.
FT   REPEAT       96    117       LRR 2.
FT   DOMAIN      197    282       IG-LIKE C2-TYPE 1.
FT   DOMAIN      295    365       IG-LIKE C2-TYPE 2.
FT   DOMAIN      538    807       PROTEIN KINASE.
FT   NP_BIND     544    552       ATP (BY SIMILARITY).
FT   BINDING     572    572       ATP (BY SIMILARITY).
FT   ACT_SITE    676    676       BY SIMILARITY.
FT   DISULFID     32     38
FT   DISULFID     36     45
FT   DISULFID    152    176
FT   DISULFID    154    194
FT   DISULFID    218    266
FT   DISULFID    302    345
FT   MOD_RES     516    516       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     702    702       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     706    706       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     707    707       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     817    817       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   SITE        516    516       INTERACTION WITH SHC PROTEIN
FT                                 (BY SIMILARITY).
FT   SITE        817    817       INTERACTION WITH PLC-GAMMA-1
```

Query Match 50.6%; Score 2277; DB 1; Length 822;
Best Local Similarity 53.7%; Pred. No. 1.4e-132;
Matches 467; Conservative 110; Mismatches 199; Indels 94; Gaps 18;

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Qy          7 PAKCSFWRIFLLGSVWLDYVG---SVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDS 62
              ||    |     |  ||  ||   :  ||| :| || : | |   |  | : || ||
Db         10 PAMARLW-----GFCWL-VVGFWRAAFACPTSCKCSASRIWCSDPSPGIVAFPRLEP--- 60

Qy         63 GNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRA 122
                        |  |   ||| | | | : |  :|  |:| | ||: ||| :|||: :  :|
Db         61 ---------NSVD-PENITEIFIANQKRLEIINEDDVEAYVGLRNLTIVDSGLKFVAHKA 110

Qy        123 FAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKL 182
              | || :|::|| : |:||:|| : |: | | || |  | | ||||| |::  ||  ::
Db        111 FLKNSNLQHINFTRNKLTSLSRKHFRHLDLSELILVGNPFTCSCDIMWIKTLQE-AKSSP 169

Qy        183 NSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVD 242
              ::|:|||:|     :||  : |  | ||  :::  |||| || :  ::|: :| |:|::
Db        170 DTQDLYCLNESSKNIPLANLQIPNCGLPSANLAAPNLTVEEGKSITLSCSVAGDPVPNMY 229

Qy        243 WIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVY 302
              | |  | |      ::| |:    :| : |::|:|:|  ::|:|||:||    || |||:
Db        230 WDVGNLVS-----KHMNETSHTQGSLRITNISSDDSGKQISCVAENLVGEDQDSVNLTVH 284

Qy        303 YPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKII--------HVEYYQ 354
              : | :  || |       || | |:||| | | | :||  | ||| |        | ||:
Db        285 FAPTITFLESPTSDHHWCIPFTVKGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYH- 343

Qy        355 EGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEP---------FPESTD 405
                  |||  : ||| |||:|||||||   |   : |: ||:  |         :|:
Db        344 ------GCLQLDNPTHMNNGDYTLIAKNEYGKDEKQISAHFMGWPGIDDGANPNYPD--- 394

Qy        406 NFILFDEV--------------SPTPPITVTHKPEEDTFGVSIAVGLAAFA--CVLLVVL 449
                :::::              :  |   || |  :  |   | :|:    | |||:|
Db        395 --VIYEDYGTAANDIGDTTNRSNEIPSTDVTDKTGREHLSVYAVVVIASVVGFC-LLVML 451

Qy        450 FVMINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIP 509
              |::  |  | |||||||| :||| ::|||||||||::|  |||| : ||| |:||||:||
Db        452 FLL--KLARHSKFGMKGPASVISNDDDSASPLHHISNGSNTPSSSEGGPDAVIIGMTKIP 509

Qy        510 VIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLV 569
              ||||||||   ::  ||||:|||||| :|||||||||||||||||| | :||:||
Db        510 VIENPQYFGITNSQLKPDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLCPEQDKILV 569

Qy        570 AVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFL 629
              ||| |||  :  ||||| |||||||||||||||||||| :|||||||||||||||||||
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Db        570 AVKTLKDASDNARKDFHREAELLTNLQHEHIVKFYGVCVEGDPLIMVFEYMKHGDLNKFL 629

Qy        630 RAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGA 689
              |||||||::: :| |      ||  ||||||| |||:|||||||||||||||||||||||
Db        630 RAHGPDAVLMAEGNP---PTELTQSQMLHIAQQIAAGMVYLASQHFVHRDLATRNCLVGE 686

Qy        690 NLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTT 749
              ||||||||||||||||||||||              |||||||||||||||||||||||||
Db        687 NLLVKIGDFGMSRDVYSTDYYR-------------VGGHTMLPIRWMPPESIMYRKFTT 732

Qy        750 ESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQR 809
              |||||| ||:|||||||||||||:|||| ||||||||||||:||| ||:|||::|||||||
Db        733 ESDVWSLGVVLWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPQEVYELMLGCWQR 792

Qy        810 EPQQRLNIKEIYKILHALGKATPIYLDILG 839
              ||  | ||| |: :|  | ||:|:||||||
Db        793 EPHMRKNIKGIHTLLQNLAKASPVYLDILG 822
```

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RESULT 9
TRKA_CHICK
ID   TRKA_CHICK     STANDARD;      PRT;   778 AA.
AC   Q91009;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   High affinity nerve growth factor receptor precursor (EC 2.7.1.112)
DE   (Trk-A) (Fragment).
GN   TRKA.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Sympathetic ganglion;
RX   MEDLINE=97047187; PubMed=8892107;
RA   Backstrom A., Soderstrom S., Kylberg A., Ebendal T.;
RT   "Molecular cloning of the chicken trkA and its expression in early
RT   peripheral ganglia.";
RL   J. Neurosci. Res. 46:67-81(1996).
CC   -!- FUNCTION: REQUIRED FOR HIGH-AFFINITY BINDING TO NERVE GROWTH
CC       FACTOR (NGF), NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT BRAIN-
CC       DERIVED NEUROTROPHIC FACTOR (BDNF). KNOWN SUBSTRATES FOR THE TRK
CC       RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1 (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC       AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=1;
CC         Comment=2 isoforms are produced;
CC       Name=1;
CC         IsoId=Q91009-1; Sequence=Displayed;
CC   -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE CONDENSING DORSAL ROOT
CC       GANGLIA AT EMBRYONAL DAY 3, AND IN THE PRIMARY SYMPATHETIC CHAIN
CC       GANGLIA AT EMBRYONAL DAY 4.
CC   -!- PTM: Ligand-mediated auto-phosphorylation (By similarity).
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
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DR   EMBL; X93581; CAA63785.1; -.
DR   HSSP; P11362; 1FGK.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; Recepttyrkinsll.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW   Receptor; Transmembrane; Glycoprotein; Repeat; Leucine-rich repeat;
KW   Immunoglobulin domain; Neurogenesis; Signal; Alternative splicing.
FT   NON_TER       1      1
FT   SIGNAL        <1     14       POTENTIAL.
FT   CHAIN         15     778      HIGH AFFINITY NERVE GROWTH FACTOR
FT                                 RECEPTOR.
FT   DOMAIN        15     400      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      401    421      POTENTIAL.
FT   DOMAIN        422    778      CYTOPLASMIC (POTENTIAL).
FT   REPEAT        69     92       LRR 1.
FT   REPEAT        94     116      LRR 2.
FT   DOMAIN        175    262      IG-LIKE C2-TYPE 1.
FT   DOMAIN        281    347      IG-LIKE C2-TYPE 2.
FT   DOMAIN        493    763      PROTEIN KINASE.
FT   NP_BIND       499    507      ATP (BY SIMILARITY).
FT   BINDING       527    527      ATP (BY SIMILARITY).
FT   ACT_SITE      633    633      BY SIMILARITY.
FT   MOD_RES       479    479      PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES       659    659      PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES       663    663      PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES       664    664      PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES       773    773      PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   SITE          479    479      INTERACTION WITH SHC PROTEIN
FT                                 (BY SIMILARITY).
FT   SITE          773    773      INTERACTION WITH PLC-GAMMA-1
FT                                 (BY SIMILARITY).
FT   CARBOHYD      100    100      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      130    130      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      143    143      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      151    151      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      194    194      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      234    234      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      262    262      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      300    300      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      320    320      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      340    340      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      384    384      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   778 AA;  87338 MW;  4B30CD9289A3C300 CRC64;

  Query Match           43.9%;  Score 1973.5;  DB 1;  Length 778;
  Best Local Similarity  51.6%;  Pred. No. 5.9e-114;
  Matches  428;  Conservative   92;  Mismatches  225;  Indels   85;  Gaps   16;

Qy        31 ACPANCVCSKTE-INCRRP-DDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENW 88
             |  |:| |  :  : || |    :|  || |                :   | : |||
Db        13 ALAAHCRCPASHTLRCREPLTVSSLSALLLG----------------AHRPTDVIIENQ 55

Qy        89 RSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQ 148
                | :|   |  :   |: ||| ||||: |   ||  |  | ::||| | ||:|||: ||

Db        56 ALLTSLTRDDTRMLWDLRHLTISNSGLQYISDDAFQDNHRLSHVNLSFNALTSLSWKTFQ 115

Qy       149 TLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQL-PLFRMNISQC 207
               | |:|| || | ||||| |||:|||    |:| :|:| |   :|| |  |    :  |
Db       116 HLPLQELTLEGNPFNCSCGIRWLQLWQNGSRAELGNQSLLC--WEGSMLVALDSHPLHDC 173

Qy       208 DLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAIN 267
             : |   :  | :: :|:||:  :||:  | |    :|::  : |  :       |  | ||
Db       174 EPPTARIEHPDVVLRQGDSVNLTCHIWGEPSATGEWVLPHVGSEPSVTKLSEWELVLEIN 233

Qy       268 LTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRG 327
                |::|  |   ||| ||| ||::  || | | :|| :: | |   :   || | |
Db       234 ----NISSSLNHKDLTCRAENSVGLAEDSVMLNVTFPPVILLLSEAIPQHFWCIPFSVDS 289

Qy       328 NPPPTLHWLHNGQPLRESKIIH---VEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPL 384
             || | : || ||  | |   ||   |||      :  |||  |:||| |||||||: :|||
Db       290 NPTPRILWLFNGSMLPEGPYIHTRIVEYEPNSTVLHGCLQLNRPTHVNNGNYTLVVQNPL 349

Qy       385 GTANQTINGHFLKEPFPESTDNFILFDEVSPTPPITVTHKP---------------EEDT 429
             | | ::| | |:  ||              ||  | | |:  |                 :| |
Db       350 GRAARSIQGRFMDNPF----------SFSPEEPIPVSISPLGTRNSSLEGPVETADEHT 398

Qy       430 FGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGIT 489
             ||||:|| || || : | |: : :|| | |||||:    ||:: |:  |  || :  | :
Db       399 FGVSVAVALAVFASLFLSVMLIALNKCGHRSKFGINRS-AVLAPEDGLAMSLHFMTLGSS 457

Qy       490 TPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAF 549
               || ::  | :     :  |||||||    |  :  | |::|||||| |||||||
Db       458 PVSSTESKLDGL-----KSNFIENPQYF-----C---NACVHHVQRRDIVLKWELGEGAF 504

Qy       550 GKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGD 609
             |||||||| :| | ::| |||||||| | || |||||||||| |||||||||||| :
Db       505 GKVFLAECSHLLPEQEKTLVAVKALKEVTENARLDFQREAELLTVLQHEHIVKFYGVCTE 564

Qy       610 GDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVY 669
             |||||||||||||||||:|||:|||||  ||   ||   |  |:|  ||  ||  ||:||||||
Db       565 GDPLIMVFEYMKHGDLNRFLRSHGPDAKILDQGQ-GQPCGQLTLSHMLQIATQIASGMVY 623

Qy       670 LASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGH 729
             ||| |||||||||||||| :|:|||||||||||:|||||||                |||
Db       624 LASLHFVHRDLATRNCLVGHDLVVKIGDFGMSRDIYSTDYYR--------------VGGR 669

Qy       730 TMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVL 789
             |||||||||||||:|||||||||:|||||:||||||||||||:|||||| |||||||  |
Db       670 TMLPIRWMPPESILYRKFTTESDIWSFGVVLWEIFTYGKQPWYQLSNTEAIECITQGREL 729

Qy       790 ERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
             |||| || ||||:|  |||||||||  :|::|:  | || |  ||||||||
Db       730 ERPRTCPSEVYDIMQSCWQREPQQR-SIQDIHSRLQALVKTPPIYLDILG 778


RESULT 10
TRKA_HUMAN
ID   TRKA_HUMAN     STANDARD;      PRT;   796 AA.
AC   P04629; P08119; Q9UIU7;
DT   13-AUG-1987 (Rel. 05, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   High affinity nerve growth factor receptor precursor (EC 2.7.1.112)
DE   (TRK1 transforming tyrosine kinase protein) (p140-TrkA) (Trk-A).
GN   NTRK1 OR TRK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM TRKA-I).
RC   TISSUE=Colon;
RX   MEDLINE=89181575; PubMed=2927393;
RA   Martin-Zanca D., Oskam R., Mitra G., Copeland T.D., Barbacid M.;
RT   "Molecular and biochemical characterization of the human trk proto-
RT   oncogene.";
RL   Mol. Cell. Biol. 9:24-33(1989).
```

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95123473; PubMed=7823156;
RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,
RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;
RT "Human trks: molecular cloning, tissue distribution, and expression
RT of extracellular domain immunoadhesins.";
RL J. Neurosci. 15:477-491(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97435581; PubMed=9290260;
RA Indo Y., Mardy S., Tsuruta M., Karim M.A., Matsuda I.;
RT "Structure and organization of the human TRKA gene encoding a high
RT affinity receptor for nerve growth factor.";
RL Jpn. J. Hum. Genet. 42:343-351(1997).
RN [4]
RP SEQUENCE OF 399-796 FROM N.A.
RX MEDLINE=86146854; PubMed=2869410;
RA Martin-Zanca D., Hughes S.H., Barbacid M.;
RT "A human oncogene formed by the fusion of truncated tropomyosin and
RT protein tyrosine kinase sequences.";
RL Nature 319:743-748(1986).
RN [5]
RP SEQUENCE OF 399-796 FROM N.A.
RX MEDLINE=88196074; PubMed=2966065;
RA Kozma S.C., Redmond S.M.S., Saurer S.M., Groner B., Hynes N.E.;
RT "Activation of the receptor kinase domain of the trk oncogene by
RT recombination with two different cellular sequences.";
RL EMBO J. 7:147-154(1988).
RN [6]
RP FUNCTION.
RX MEDLINE=91218846; PubMed=1850821;
RA Hempstead B.L., Martin-Zanca D., Kaplan D.R., Parada L.F., Chao M.V.;
RT "High-affinity NGF binding requires coexpression of the trk proto-
RT oncogene and the low-affinity NGF receptor.";
RL Nature 350:678-683(1991).
RN [7]
RP FUNCTION.
RX MEDLINE=91191557; PubMed=1849459;
RA Klein R., Jing S., Nanduri V., O'Rourke E., Barbacid M.;
RT "The trk proto-oncogene encodes a receptor for nerve growth factor.";
RL Cell 65:189-197(1991).
RN [8]
RP ALTERNATIVE SPLICING.
RX MEDLINE=93315496; PubMed=8325889;
RA Barker P.A., Lomen-Hoerth C., Gensch E.M., Meakin S.O., Glass D.J.,
RA Shooter E.M.;
RT "Tissue-specific alternative splicing generates two isoforms of the
RT trkA receptor.";
RL J. Biol. Chem. 268:15150-15157(1993).
RN [9]
RP MUTAGENESIS OF TYR-791.
RX MEDLINE=94179299; PubMed=7510697;
RA Loeb D.M., Stephens R.M., Copeland T.D., Kaplan D.R., Greene L.A.;
RT "A Trk nerve growth factor (NGF) receptor point mutation affecting
RT interaction with phospholipase C-gamma 1 abolishes NGF-promoted
RT peripherin induction but not neurite outgrowth.";
RL J. Biol. Chem. 269:8901-8910(1994).
RN [10]
RP MUTAGENESIS, AND PHOSPHORYLATION SITES.
RX MEDLINE=94206546; PubMed=8155326;
RA Stephens R.M., Loeb D.M., Copeland T.D., Pawson T., Greene L.A.,
RA Kaplan D.R.;
RT "Trk receptors use redundant signal transduction pathways involving
RT SHC and PLC-gamma 1 to mediate NGF responses.";
RL Neuron 12:691-705(1994).
RN [11]
RP STRUCTURE BY NMR OF 489-500.
RX MEDLINE=96097066; PubMed=8524391;
RA Zhou M.M., Ravichandran K.S., Olejniczak E.F., Petros A.M.,
RA Meadows R.P., Sattler M., Harlan J.E., Wade W.S., Burakoff S.J.,
RA Fesik S.W.;
RT "Structure and ligand recognition of the phosphotyrosine binding
RT domain of Shc.";
RL Nature 378:584-592(1995).
RN [12]
RP VARIANT CIPA ARG-577.
RX MEDLINE=96331294; PubMed=8696348;
RA Indo Y., Tsuruta M., Hayashida Y., Karim M.A., Ohta K., Kawano T.,
RA Mitsubuchi H., Tonoki H., Awaya Y., Matsuda I.;
RT "Mutations in the TRKA/NGF receptor gene in patients with congenital
RT insensitivity to pain with anhidrosis.";
RL Nat. Genet. 13:485-488(1996).
RN [13]
RP VARIANT CIPA PRO-780.
RX MEDLINE=99192367; PubMed=10090906;
RA Greco A., Villa R., Tubino B., Romano L., Penso D., Pierotti M.A.;
RT "A novel NTRK1 mutation associated with congenital insensitivity to
RT pain with anhidrosis.";
RL Am. J. Hum. Genet. 64:1207-1210(1999).
RN [14]
RP VARIANTS CIPA PRO-213; TRP-649 AND SER-714, AND VARIANTS SER-85;
RP TYR-604 AND VAL-613.
RX MEDLINE=99264238; PubMed=10330344;
RA Mardy S., Miura Y., Endo F., Matsuda I., Sztriha L., Frossard P.,
RA Moosa A., Ismail E.A.R., Macaya A., Andria G., Toscano E., Gibson W.,
RA Graham G.E., Indo Y.;
RT "Congenital insensitivity to pain with anhidrosis: novel mutations in
RT the TRKA (NTRK1) gene encoding a high-affinity receptor for nerve
RT growth factor.";
RL Am. J. Hum. Genet. 64:1570-1579(1999).
RN [15]
RP VARIANTS TYR-604; VAL-613 AND GLN-780.
RX MEDLINE=99371280; PubMed=10443680;
RA Gimm O., Greco A., Hoang-Vu C., Dralle H., Pierotti M.A., Eng C.;
RT "Mutation analysis reveals novel sequence variants in NTRK1 in
RT sporadic human medullary thyroid carcinoma.";
RL J. Clin. Endocrinol. Metab. 84:2784-2787(1999).
RN [16]
RP VARIANT CIPA VAL-587.
RX MEDLINE=99250414; PubMed=10233776;
RA Yotsumoto S., Setoyama M., Hozumi H., Mizoguchi S., Fukumaru S.,
RA Kobayashi K., Saheki T., Kanzaki T.;
RT "A novel point mutation affecting the tyrosine kinase domain of the
RT TRKA gene in a family with congenital insensitivity to pain with
RT anhidrosis.";
RL J. Invest. Dermatol. 112:810-814(1999).
RN [17]
RP VARIANTS TYR-604 AND VAL-613.
RX MEDLINE=99318093; PubMed=10391209;
RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions
RT of human genes.";
RL Nat. Genet. 22:231-238(1999).
RN [18]
RP ERRATUM.
RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RL Nat. Genet. 23:373-373(1999).
RN [19]
RP VARIANT CIPA LEU-695, AND VARIANT VAL-613.
RC TISSUE=Peripheral blood;
RX MEDLINE=20321341; PubMed=10861667;
RA Shatzky S., Moses S., Levy J., Pinsk V., Hershkovitz E., Herzog L.,
RA Shorer Z., Luder A., Parvari R.;
RT "Congenital insensitivity to pain with anhidrosis (CIPA) in
RT Israeli-Bedouins: genetic heterogeneity, novel mutations in the
RT TRKA/NGF receptor gene, clinical findings, and results of nerve
RT conduction studies.";
RL Am. J. Med. Genet. 92:353-360(2000).

```
RN   [20]
RP   VARIANTS CIPA PRO-93; ARG-522; ARG-577; CYS-654 AND TYR-674.
RX   MEDLINE=20435070; PubMed=10982191;
RA   Miura Y., Mardy S., Awaya Y., Nihei K., Endo F., Matsuda I., Indo Y.;
RT   "Mutation and polymorphism analysis of the TRKA (NTRK1) gene encoding
RT   a high-affinity receptor for nerve growth factor in congenital
RT   insensitivity to pain with anhidrosis (CIPA) families.";
RL   Hum. Genet. 106:116-124(2000).
RN   [21]
RP   VARIANT CIPA ARG-577.
RX   MEDLINE=20036616; PubMed=10567924;
RA   Greco A., Villa R., Fusetti L., Orlandi R., Pierotti M.A.;
RT   "The Gly571Arg mutation, associated with the autonomic and sensory
RT   disorder congenital insensitivity to pain with anhidrosis, causes the
RT   inactivation of the NTRK1/nerve growth factor receptor.";
RL   J. Cell. Physiol. 182:127-133(2000).
CC   -!- FUNCTION: REQUIRED FOR HIGH-AFFINITY BINDING TO NERVE GROWTH
CC       FACTOR (NGF), NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT BRAIN-
CC       DERIVED NEUROTROPHIC FACTOR (BDNF). KNOWN SUBSTRATES FOR THE TRK
CC       RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1. HAS A CRUCIAL
CC       ROLE IN THE DEVELOPMENT AND FUNCTION OF THE NOCICEPTIVE RECEPTION
CC       SYSTEM AS WELL AS ESTABLISHMENT OF THERMAL REGULATION VIA
CC       SWEATING. ACTIVATES ERK1 BY EITHER SHC- OR PLC-GAMMA-1-DEPENDENT
CC       SIGNALING PATHWAY.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC       AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Both isoforms have similar biological properties;
CC       Name=TrkA-II;
CC         IsoId=P04629-1; Sequence=Displayed;

  Query Match             43.6%;  Score 1961;  DB 1;  Length 796;
  Best Local Similarity   49.5%;  Pred. No. 3.6e-113;
  Matches  420;  Conservative  103;  Mismatches  228;  Indels   98;  Gaps   17;

Qy         22 WLDYVGSVLA-----------CP-ANCVCSKTEINCRRPDDGNLFPL--LEGQDSGNSNG 67
Db         15 WAAGPGSLLAWLILASAGAAPCPDACCPHGSSGLRCTR--DGALDSLHHLPG-------- 64

Qy         68 NANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNP 127
Db         65 ---------AENLTELYIENQQHLQHLELRDLRGLGELRNLTIVKSGLRFVAPDAFHFTP 115

Qy        128 HLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNL 187
Db        116 RLSRLNLSFNALESLSWKTVQGLSLQELVLSGNPLHCSCALRWLQRWEEEGLGGVPEQKL 175

Qy        188 YCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTG 247
Db        176 QC----HGQGPLAHMPNASCGVPTLKVQVPNASVDVGDDVLLRCQVEGRGLEQAGWILTE 231

Qy        248 LQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRV 307
Db        232 LEQ---SATVMKSGGLPSLGLTLANVTSDLNRKNLTCWAENDVGRAEVSVQVNVSFPASV 288

Qy        308 VSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEG---EISEGCLL 364
Db        289 QLHTAVEMH-HWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCLR 347

Qy        365 FNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPITVTHK 424
Db        348 LNQPTHVNNGNYTLLAANPFGQASASIMAAFMDNPF-----------EFNPEDPIPVSFS 396

Qy        425 P--------------EEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAV 470
Db        397 PVDTNSTSGDPVEKKDETPFGVSVAVGLAVFACLFLSTLLLVLNKCGRRNKFGINRP-AV 455

Qy        471 ISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYV 530
Db        456 LAPEDGLAMSLHFMTLGGSSLSPTE-GKGSGLQG----HIIENPQYF--------SDACV 502

Qy        531 QHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAE 590
Db        503 HHIKRRDIVLKWELGEGAFGKVFLAECHNLLPEQDKMLVAVKALKEASESARQDFQREAE 562

Qy        591 LLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGE 650
Db        563 LLTMLQHQHIVRFFGVCTEGRPLLMVFEYMRHGDLNRFLRSHGPDAKLLAGGED-VAPGP 621

Qy        651 LGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYY 710
Db        622 LGLGQLLAVASQVAAGMVYLAGLHFVHRDLATRNCLVGQGLVVKIGDFGMSRDIYSTDYY 681

Qy        711 RLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQP 770
Db        682 R--------------VGGRTMLPIRWMPPESILYRKFTTESDVWSFGVVLWEIFTYGKQP 727

Qy        771 WFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKA 830
Db        728 WYQLSNTEAIDCITQGRELERPRACPPEVYAIMRGCWQREPQQRHSIKDVHARLQALAQA 787

Qy        831 TPIYLDILG 839
Db        788 PPVYLDVLG 796


RESULT 11
TRKA_RAT
ID   TRKA_RAT       STANDARD;      PRT;   799 AA.
AC   P35739;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   High affinity nerve growth factor receptor precursor (EC 2.7.1.112)
DE   (p140-TrkA) (Slow nerve growth factor receptor) (Trk-A).
GN   NTRK1 OR TRKA OR TRK.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM TRKA-II).
RX   MEDLINE=92196121; PubMed=1312719;
RA   Meakin S.O., Suter U., Drinkwater C.C., Welcher A.A., Shooter E.M.;
RT   "The rat trk protooncogene product exhibits properties characteristic
RT   of the slow nerve growth factor receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:2374-2378(1992).
RN   [2]
RP   ALTERNATIVE SPLICING.
RX   MEDLINE=93315496; PubMed=8325889;
RA   Barker P.A., Lomen-Hoerth C., Gensch E.M., Meakin S.O., Glass D.J.,
RA   Shooter E.M.;
RT   "Tissue-specific alternative splicing generates two isoforms of the
RT   trkA receptor.";
RL   J. Biol. Chem. 268:15150-15157(1993).
CC   -!- FUNCTION: REQUIRED FOR HIGH-AFFINITY BINDING TO NERVE GROWTH
CC       FACTOR (NGF), NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT BRAIN-
CC       DERIVED NEUROTROPHIC FACTOR (BDNF). KNOWN SUBSTRATES FOR THE TRK
CC       RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1. HAS A CRUCIAL
CC       ROLE IN THE DEVELOPMENT AND FUNCTION OF THE NOCICEPTIVE RECEPTION
CC       SYSTEM AS WELL AS ESTABLISHMENT OF THERMAL REGULATION VIA
CC       SWEATING. ACTIVATES ERK1 BY EITHER SHC- OR PLC-GAMMA-1-DEPENDENT
CC       SIGNALING PATHWAY (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC       AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Both isoforms have similar biological properties;
CC       Name=TrkA-II;
```

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CC         IsoId=P35739-1; Sequence=Displayed;
CC       Name=TrkA-I;
CC         IsoId=P35739-2; Sequence=VSP_002900;
CC   -!- TISSUE SPECIFICITY: TRKA-II IS PRIMARILY EXPRESSED IN NEURONAL
CC       CELLS; TRKA-I IS FOUND IN NON-NEURONAL TISSUES.
CC   -!- PTM: Ligand-mediated auto-phosphorylation.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M85214; AAA42286.1; -.
DR   EMBL; L12225; -; NOT_ANNOTATED_CDS.
DR   PIR; A41981; TVRTTB.
DR   HSSP; P11362; 1FGK.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW   Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW   Leucine-rich repeat; Immunoglobulin domain; Neurogenesis;
KW   Alternative splicing.
FT   SIGNAL        1     32       POTENTIAL.
FT   CHAIN        33    799       HIGH AFFINITY NERVE GROWTH FACTOR
FT                                 RECEPTOR.
FT   DOMAIN       33    418       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    419    442       POTENTIAL.
FT   DOMAIN      443    799       CYTOPLASMIC (POTENTIAL).
FT   REPEAT       90    113       LRR 1.
FT   REPEAT      114    137       LRR 2.
FT   DOMAIN      196    285       IG-LIKE C2-TYPE 1.
FT   DOMAIN      295    368       IG-LIKE C2-TYPE 2.
FT   DOMAIN      513    784       PROTEIN KINASE.
FT   NP_BIND     519    527       ATP (BY SIMILARITY).
FT   BINDING     547    547       ATP (BY SIMILARITY).
FT   ACT_SITE    653    653       BY SIMILARITY.
FT   MOD_RES     499    499       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     679    679       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     683    683       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     684    684       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     794    794       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   SITE        499    499       INTERACTION WITH SHC PROTEIN
FT                                 (BY SIMILARITY).
FT   SITE        794    794       INTERACTION WITH PLC-GAMMA-1
FT                                 (BY SIMILARITY).
FT   CARBOHYD     67     67       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    121    121       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    190    190       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    204    204       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    255    255       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    264    264       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    320    320       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    325    325       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    341    341       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    361    361       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    404    404       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    396    401       Missing (in isoform TrkA-I).
FT                                 /FTId=VSP_002900.
SQ   SEQUENCE   799 AA;  87868 MW;  D564E8801E8978F8 CRC64;

  Query Match             42.5%;  Score 1913;  DB 1;  Length 799;
  Best Local Similarity   48.2%;  Pred. No. 3.2e-110;
  Matches  403;  Conservative  115;  Mismatches  230;  Indels   88;  Gaps   14;

Qy         29 VLACPANCVCSKT-------EINCRRPDDGNLFPLLEGQDSGNSNGNANINITDISRNIT 81
              :|||     | :|         : | |   |  | |                   : |:|
Db         27 MLACACAASCRETCCPVGPSGLRCTRAGTLNTLRGLRG----------------AGNLT 69

Qy         82 SIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTT 141
               :::|| | |  |   |::   |: |||  |||| : | ||   | | ::|||| | :
Db         70 ELYVENQRDLQRLEFEDLQGLGELRSLTIVKSGLRFVAPDAPHFTPRLSHLNLSSNALES 129

Qy        142 LSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQLPLFR 201
              |||:  | |||::| |  |  :||| : |:| |:::    : :| |    :   |||
Db        130 LSWKTVQGLSLQDLTLSGNPLHCSCALLWLQRWEQEDLCGVYTQKLQGSGSGDQFLPLGH 189

Qy        202 MNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWT 261
              |  | :| : :   | :|  ||:  : |   |  |   |||:| |:   | : :
Db        190 NN--SCGVPSVKIQMPNDSVEVGDDVFLQCQVEGQALQQADWILTELEGTATMKKS---G 244

Qy        262 NVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCI 321
              :: :: |||||||: |   :|| ||| || :  || ::| :|   | | :   :  ||
Db        245 DLPSLGLTLVNVTSDLNKKNVTCWAENDVGRAEVSVQVSVSPPAS-VHLGKAVEQHHWCI 303

Qy        322 EFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE----GCLLFNKPTHYNNGNYT 377
              | | | | |:| |  ||  | |:  |  :: :    :|    |||  |:||| ||||||
Db        304 PFSVDGQPAPSLRWFFNGSVLNETSFIFTQFLESALTNETMRHGCLRLNQPTHVNNGNYT 363

Qy        378 LIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPITVTHKP------------ 425
              |:| || | |  :|   |:  ||            | :|  || |:  |
Db        364 LLAANPYGQAAASIMAAFMDNPF-----------EFNPEDPIPVSFSPVDTNSTSRDPVE 412

Qy        426 --EEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASPLHH 483
                :|  ||||:|||||   | : |  | :::|| |:|||||:  | ||:: |:  |  ||
Db        413 KKDETPFGVSVAVGLAVSAALFLSALLLVLNKCGQRSKFGINRP-AVLAPEDGLAMSLHF 471

Qy        484 INHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRE 543
              :  | :: |  : |  : : |     ::|||||          || | ||||:||:|| |
Db        472 MTLGGSSLSPTE-GKGSGLQG----HIMENPQYF--------SDTCVHHIKRQDIILKWE 518

Qy        544 LGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHIVKF 603
              |||||||||||||||||   :|||||||||||: :  ||:|| |||||| |||:|||:|
Db        519 LGEGAFGKVFLAECYNLLNDQDKMLVAVKALKETSENARQDFHREAELLTMLQHQHIVRF 578

Qy        604 YGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIASQI 663
              :||| :| ||:||||||:|||||:|||:|||||  :|   :  | | ||| |:| :|||:
Db        579 FGVCTEGGPLLMVFEYMRHGDLNRFLRSHGPDAKLLAGGED-VAPGPLGLGQLLAVASQV 637

Qy        664 ASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIW 723
              |:|||||| ||||||||||||||  |:||||||||||:|||||||
Db        638 AAGMVYLASLHFVHRDLATRNCLVGQGLVVKIGDFGMSRDIYSTDYYR------------ 685

Qy        724 CEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECI 783
                ||| ||||||||||||:||||:|||||||||:|||||||||||:|||||| ||||
Db        686 --VGGRTMLPIRWMPPESILYRKFSTESDVWSFGVVLWEIFTYGKQPWYQLSNTEAIECI 743

Qy        784 TQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||| ||||| || :|| :| ||||||||||::|:::  | || :| | |||:||
Db        744 TQGRELERPRACPPDVYAIMRGCWQREPQQRLSMKDVHARLQALAQAPPSYLDVLG 799
```

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RESULT 12
TRK1_LYMST
ID   TRK1_LYMST     STANDARD;      PRT;   794 AA.
AC   O76997;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Putative neurotrophin receptor LTRK 1 precursor (EC 2.7.1.112).
OS   Lymnaea stagnalis (Great pond snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC   Lymnaeoidea; Lymnaeidae; Lymnaea.
OX   NCBI_TaxID=6523;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98232499; PubMed=9564036;
RA   van Kesteren R.E., Fainzilber M., Hauser G., van Minnen J.,
RA   Vreugdenhil E., Smit A.B., Ibanez C.F., Geraerts W.P.M.,
RA   Bulloch A.G.M.;
RT   "Early evolutionary origin of the neurotrophin receptor family.";
RL   EMBO J. 17:2534-2542(1998).
CC   -!- FUNCTION: MAY BIND AN ENDOGENOUS INVERTEBRATE NEUROTROPHIN. BINDS
CC       HUMAN NT-3, BUT NOT NGF OR BDNF.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSION IS CONFINED TO THE CENTRAL NERVOUS
CC       SYSTEM AND ITS ASSOCIATED ENDOCRINE TISSUES.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC       receptor subfamily.
CC   -!- SIMILARITY: Contains 2 leucine-rich (LRR) repeats.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U61728; AAC26840.1; -.
DR   HSSP; P08631; 1AD5.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR003591; LRR_typ.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00369; LRR_TYP; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   Transferase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
KW   Phosphorylation; Receptor; Glycoprotein; Neurogenesis;
KW   Leucine-rich repeat; Repeat; Signal.
FT   SIGNAL        1     33       POTENTIAL.
FT   CHAIN        34    794       PUTATIVE NEUROTROPHIN RECEPTOR LTRK 1.
FT   DOMAIN       34    419       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    420    440       POTENTIAL.
FT   DOMAIN      441    794       CYTOPLASMIC (POTENTIAL).
FT   REPEAT      181    204       LRR 1.
FT   REPEAT      205    228       LRR 2.
FT   DOMAIN      504    775       PROTEIN KINASE.
FT   NP_BIND     510    518       ATP (BY SIMILARITY).
FT   BINDING     538    538       ATP (BY SIMILARITY).
FT   ACT_SITE    647    647       BY SIMILARITY.
FT   CARBOHYD     64     64       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    102    102       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    128    128       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    288    288       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    374    374       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MOD_RES     673    673       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     677    677       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     678    678       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES     789    789       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ   SEQUENCE   794 AA;  89054 MW;  FFF3EF5766E1A440 CRC64;

  Query Match             25.6%;  Score 1150.5;  DB 1;  Length 794;
  Best Local Similarity   33.8%;  Pred. No. 2.4e-63;
  Matches  290;  Conservative  111;  Mismatches  269;  Indels  189;  Gaps   22;

Qy          2 DVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTE----INCRRPDDGNLFPLL 57
              : ::   |||           |    |  ||||:| |: |     ::|  ||    ||::
Db        102 NTTMAGTKCS----------LQVDLSTFACPADCQCNATSEGMVVSCVTPDTLREFPVI 150

Qy         58 EGQDSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRS 117
                          :::| :  : :     | :|   ::: :| |: |||:| || :
Db        151 --------------AREVARAVIKLELRGQSKLTSLK-TELKFFTCLKHLTIENCGLNN 194

Qy        118 IQPRAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQ 177
              ||  ||      |  |||  | ||     :| :||:|||| || |   |||       ||
Db        195 IQGIAFKTLTSLETINLRHNHLTEFPQELLRTLNLRELWLEGNALTCSC----TNLWLRS 250

Qy        178 GEAKLNSQNLYCINADG-SQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGS 236
               :   :  : |   || |:: : :     | :|:|
Db        251 VDVAADRSEMTCSTRDGVSKMKMTQFKCEPCGIPDIR----------------------- 287

Qy        237 PLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNAS 296
                                          |:||  |    ||  |
Db        288 ----------------------------NMTL--VFEPKNGMFL-------------- 301

Qy        297 VALTVYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRES-----KIIHVE 351
                                    : ||: | | | :  | |   :  |     |:   :
Db        302 ------------------------LRFVISGCPKPKIDLLRNHHHVLRSGSSQFKLTDFK 337

Qy        352 YYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFD 411
                  |::  | :         :   | | | |  | ||||    |   :  | |: :  |
Db        338 SEFNGQVVTGTITILPHMETSQTTYVLTAVNSKGQANQTF--HLYDQTTPASSIHIPL-- 393

Qy        412 EVSPTPP-----ITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKG 466
              |  ||       |    | || ||    | |      |:|::  | |    :|:|
Db        394 --SNIPPRISSATTPRASPTED-FGPQTQVILPVVGVVILLISAVFIIYLCQRAK----- 445

Qy        467 PVAVISGEEDSASPLHHINHG--ITTPSSLDAGPDTVVIG--MTRIPVIENPQYFRQGHN 522
                           | :|      : ||   :    |  :| : :::|| |
Db        446 ---------------HRSHARQRCKKALLDKKFNEFQEGVPLTGLQLVDNPNY-NLTKK 488

Qy        523 CHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDP-TLAA 581
              |   |  : :: : |:| | :|||||:|||  | :|    :  :||||  ||   : :
Db        489 KHVATTCPKTVRLQTILLMRVIGEGAFGRVFLGTCAHLIQKNEFAIVAVKTLKGSCSDSL 548

Qy        582 RKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVD 641
              ::||:||||:|  ::| :|| ||||| : |  :|:||:|::|||||:|| |||||  | |
Db        549 KRDFEREAEMLATIEHANIVTFYGVCTESDQWMMIFEFMENGDLNKYLRMHGPDAAFLKD 608

Qy        642 GQPRQA-KGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGM 700
                : :|:|   |:: |  |||| | ||| ||||||||||||||| :|:|:|||||
Db        609 RDSMDSDEGQLTREQLMKIVLQIASAMEYLALQHFVHRDLATRNCLVGCDLVVKLGDFGM 668

Qy        701 SRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVIL 760
              |||||:|||||              | |  |||:||||||||:|| ||||||||||| |
Db        669 SRDVYTTDYYR--------------VEGTAMLPVRWMPPESIIYRTFTTESDVWSFGVTL 714

Qy        761 WEIFTYGKQPWFQLSNTEVIECITQGRVLER-PRVCPKEVYDVMLGCWQREPQQRLNIKE 819
              ||:|||||||||: ||:|||| |   | |:| || |   || || |||:  || || :|:
Db        715 WEVFTYGKQPWFEYSNSEVIEHIKNSRTLKRPPRTCTDGVYRVMQGCWKPNPQDRLTMKD 774

Qy        820 IYKILHALGKATPIYLDIL 838
              | ::|       |:|:||:
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Db        775 IAELLREEVSGDPVYIDII 793


RESULT 13
ROR1_DROME
ID   ROR1_DROME     STANDARD;      PRT;   685 AA.
AC   Q24488;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Tyrosine-protein kinase transmembrane receptor Ror precursor
DE   (EC 2.7.1.112) (dRor).
GN   ROR OR CG4926.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC   STRAIN=Canton-S; TISSUE=Larval brain;
RX   MEDLINE=93348222; PubMed=8394009;
RA   Wilson C., Goberdhan D.C.I., Steller H.;
RT   "Dror, a potential neurotrophic receptor gene, encodes a Drosophila
RT   homolog of the vertebrate Ror family of Trk-related receptor tyrosine
RT   kinases.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [3]
RP   SEQUENCE OF 545-597 FROM N.A.
RX   MEDLINE=98401146; PubMed=9731193;
RA   Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
RT   "Sampling the genomic pool of protein tyrosine kinase genes using the
RT   polymerase chain reaction with genomic DNA.";
RL   Biochem. Biophys. Res. Commun. 249:660-667(1998).
CC   -!- FUNCTION: Tyrosine-protein kinase receptor that functions during
CC       early stages of neuronal development.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in neurons of the developing nervous
CC       system.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 frizzled (FZ) domain.
CC   -!- SIMILARITY: Contains 1 kringle domain.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; L20297; AAA28860.1; -.
DR   EMBL; AE003628; AAF52885.1; -.
DR   EMBL; AJ002908; CAA05743.1; -.
DR   PIR; A48289; A48289.
DR   HSSP; P11362; 1FGK.
DR   FlyBase; FBgn0010407; Ror.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; NAS.
DR   GO; GO:0007417; P:central nervous system development; IEP.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
DR   InterPro; IPR000024; Fz_domain.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00051; kringle; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000395; Kringle; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00130; KR; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50038; FZ; 1.
DR   PROSITE; PS00021; KRINGLE_1; 1.
DR   PROSITE; PS50070; KRINGLE_2; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   Transferase; Kinase; Tyrosine-protein kinase; ATP-binding; Receptor;
KW   Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
KW   Developmental protein.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    685       TYROSINE-PROTEIN KINASE TRANSMEMBRANE
FT                                 RECEPTOR ROR.
FT   DOMAIN       25    317       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    318    338       POTENTIAL.
FT   DOMAIN      339    685       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       36    225       FZ.
FT   DOMAIN      236    310       KRINGLE.
FT   DOMAIN      410    677       PROTEIN KINASE.
FT   NP_BIND     416    424       ATP (BY SIMILARITY).
FT   BINDING     442    442       ATP (BY SIMILARITY).
FT   ACT_SITE    539    539       BY SIMILARITY.
FT   MOD_RES     565    565       PHOSPHORYLATION (AUTO-) (BY
FT                                 SIMILARITY).
FT   MOD_RES     569    569       PHOSPHORYLATION (AUTO-) (BY
FT                                 SIMILARITY).
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FT   MOD_RES     570    570       PHOSPHORYLATION (AUTO-) (BY
FT                                SIMILARITY).
FT   CARBOHYD     45     45       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    129    129       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    144    144       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    250    250       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   685 AA;  78142 MW;  526162D27D5FD7C7 CRC64;

  Query Match             15.6%;  Score 700;  DB 1;  Length 685;
  Best Local Similarity   38.3%;  Pred. No. 9.6e-36;
  Matches  158;  Conservative   74;  Mismatches  104;  Indels   76;  Gaps   14;

Qy        428 DTFGVSIAVGLAAFACVLLVVLFVMINKYGRRS--KFGMKGPVAVISGEEDSASPLHHIN 485
              |   ::| ||  |   :: :::| :|  : ||:   :||:                :|:||
Db        312 DKIWIAI-VGTTAAIILIFIIIFAII-LFKRRTIMHYGMRN-------------IHNIN 355

Qy        486 HGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPD--------------TYVQ 531
                  |||:     |  : | ::   : | |   :|:  :  |                 :
Db        356 ----TPSA-----DKNIYGNSQ---LNNAQDAGRGNLGNLSDHVALNSKLIERNTLLRIN 403

Qy        532 HIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKD-PTLAARKDFQREAE 590
              |   :|:    ||||||||||:  :   | | |  : ||:||||:  ::  ::||:|| |
Db        404 HFTLQDVEFLEELGEGAFGKVYKGQL--LQPNKTTITVAIKALKENASVKTQQDFKREIE 461

Qy        591 LLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGE 650
              |:::|:|::||   ||  : :|  |:|||| :|||::|          |:   | : |
Db        462 LISDLKHQNIVCILGVVLNKEPYCMLFEYMANGDLHEF----------LISNSPTEGK-- 509

Qy        651 LGLSQM--LHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTD 708
                ||:  | || ||: || ||:: |:|||||| |||||   |:||| |||:|||:||:|
Db        510 -SLSQLEFLQIALQISEGMQYLSAHHYVHRDLAARNCLVNEGLVVKISDFGLSRDIYSSD 568

Qy        709 YYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGK 768
              |||               |   ::||:|||| |||:| ||||||||||||:||||::||
Db        569 YYR--------------VQSKSLLPVRWMPSESILYGKFTTESDVWSFGVVLWEIYSYGM 614

Qy        769 QPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEI 820
              ||::  || |||  |   ::|  |  ||  || :|: ||  :  :|    :|
Db        615 QPYYGFSNQEVINLIRSRQLLSAPENCPTAVYSLMIECWHEQSVKRPTFTDI 666


RESULT 14
ROR2_DROME
ID   ROR2_DROME     STANDARD;      PRT;   724 AA.
AC   Q9V6K3; O02001; O96391; Q9TYH9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Tyrosine-protein kinase transmembrane receptor Ror2 precursor
DE   (EC 2.7.1.112) (Neurospecific receptor tyrosine kinase).
GN   NRK OR ROR2 OR CG4007.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Frith K.J., Scott M.J.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [3]
RP   REVISIONS.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [4]
RP   SEQUENCE OF 17-724 FROM N.A., AND CHARACTERIZATION.
RC   TISSUE=Imaginal disks;
RX   MEDLINE=97277331; PubMed=9115253;
RA   Oishi I., Sugiyama S., Liu Z.J., Yamamura H., Nishida Y., Minami Y.;
RT   "A novel Drosophila receptor tyrosine kinase expressed specifically
RT   in the nervous system. Unique structural features and implication in
RT   developmental signaling.";
RL   J. Biol. Chem. 272:11916-11923(1997).
RN   [5]
RP   SEQUENCE OF 586-638 FROM N.A.
RX   MEDLINE=98401146; PubMed=9731193;
RA   Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
RT   "Sampling the genomic pool of protein tyrosine kinase genes using the
RT   polymerase chain reaction with genomic DNA.";
RL   Biochem. Biophys. Res. Commun. 249:660-667(1998).
CC   -!- FUNCTION: Tyrosine-protein kinase receptor that functions during
CC       early stages of neuronal development (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Expressed in neural cell lineage from
CC       embryonic stage 11 onwards, resulting in expression in the brain
CC       and ventral nerve cord at the end of embryogenesis.
CC   -!- DEVELOPMENTAL STAGE: Expressed at high levels in embryos and
CC       larvae, low levels in adults and pupae show maximal expression.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 frizzled (FZ) domain.
CC   -!- SIMILARITY: Contains 1 kringle domain.
```

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CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF037164; AAD02091.1; -.
DR   EMBL; AE003819; AAF58420.2; -.
DR   EMBL; AB001420; BAA20134.1; -.
DR   EMBL; AJ002920; CAA05755.1; -.
DR   HSSP; P11362; 1FGK.
DR   FlyBase; FBgn0020391; Nrk.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IDA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR   GO; GO:0007165; P:signal transduction; IDA.
DR   InterPro; IPR000024; Fz_domain.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF01392; Fz; 1.
DR   Pfam; PF00051; kringle; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000395; Kringle; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50038; FZ; 1.
DR   PROSITE; PS00021; KRINGLE_1; 1.
DR   PROSITE; PS50070; KRINGLE_2; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Transferase; Kinase; Tyrosine-protein kinase; ATP-binding; Receptor;
KW   Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
KW   Developmental protein.
FT   SIGNAL        1     41       POTENTIAL.
FT   CHAIN        42    724       TYROSINE-PROTEIN KINASE TRANSMEMBRANE
FT                                 RECEPTOR ROR2.
FT   DOMAIN        42    322       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     323    343       POTENTIAL.
FT   DOMAIN       344    724       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       441    711       PROTEIN KINASE.
FT   NP_BIND      447    455       ATP (BY SIMILARITY).
FT   BINDING      475    475       ATP (BY SIMILARITY).
FT   ACT_SITE     580    580       BY SIMILARITY.
FT   MOD_RES      606    606       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES      610    610       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MOD_RES      611    611       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   CONFLICT      51     51       V -> A (IN REF. 1).
FT   CONFLICT     192    192       H -> Y (IN REF. 4).
FT   CONFLICT     306    306       V -> G (IN REF. 1).
FT   CONFLICT     387    387       G -> V (IN REF. 4).
FT   CONFLICT     391    391       T -> M (IN REF. 4).
FT   CONFLICT     547    547       Q -> R (IN REF. 1 AND 4).
FT   CONFLICT     706    724       EINHCIQHSIAESECKAML -> RSTTASSTASPRASARQC
FT                                 FRGLPEK (IN REF. 4).
SQ   SEQUENCE   724 AA;  81836 MW;  0FFB9E1F7E4F6A26 CRC64;

  Query Match           14.9%;  Score 670.5;  DB 1;  Length 724;
  Best Local Similarity  32.4%;  Pred. No. 6.7e-34;
  Matches  182;  Conservative   72;  Mismatches  169;  Indels  139;  Gaps   14;

Qy        354 QEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTING-------------HFL---- 396
              :| |:|  |           |||     :  :|| | : :|             ||
Db        211 KESEVSYDC---------RNGN----GRFYMGTMNVSKSGIPCQRWDTQYPHKHFQPPLV 257

Qy        397 ----------------KEPFP-----------ESTDNFILFDEVSPTPPITVTHKPEEDT 429
                             :|| |           :  |  :  | | |       |    |
Db        258 FHQLLEGENYCRNAGGEEPHPWCYTVDESVRWQHCDIPMCPDYVDPNAVDLNTPIKMEKF 317

Qy        430 FGVSIAVGLAAFACVLLVVLFVMI---------------------------------N 454
              |  |:   ||     | :| | :||                                 |
Db        318 FTPSMIFLLAGIGFVAIVTLHLMILLVYKLSKHKDYSQPAGAATAECSVSMRGGGDCGGN 377

Qy        455 KYGRRSKFGMKGPVAVIS--GEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIE 512
                  |  | |    ::  |   | : :|     :|| :::     |
Db        378 LNTSRETLGGNGNTNTLAKWGTIRSTATIHSNCVALTTVTNVSDAKGT------------ 425

Qy        513 NPQYFRQGHNCHKPDTYVQHIK--RRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVA 570
                        ||:  :: ::  | |||  | ||:||||:|| |    | | :: :|||
Db        426 ------------KPNARLEKLEYPRGDIVYVRSLGQGAFGRVFQARAPGLVPDQEDLLVA 473

Qy        571 VKALKDPTL-AARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFL 629
              || |||      : ||:||| ||    | :||:  |||  | |: ::|||| |||::||
Db        474 VKMLKDDASDQMQMDFEREACLLAEFDHPNIVRLLGVCALGRPMCLLFEYMAPGDLSEFL 533

Qy        630 RAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGA 689
              ||  | |       | |    || | ||   |: ||:||:||: : ||||||||||:
Db        534 RACSPYATHQAPTQDRLQLNELHLLQM---AANIAAGMLYLSERKFVHRDLATRNCLINE 590

Qy        690 NLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTT 749
              :: ||| |||:|  :|  |||:       |||            :|||||| |||:| ||:
Db        591 HMAVKIADFGLSHKIYLQDYYK---GDENDF----------IPIRWMPLESILYNKFSL 636

Qy        750 ESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQR 809
              |||||::|: |||:|::  ||:| |:: ||| | :| ||  |   | || :|  || |
Db        637 ESDVWAYGICLWEVFSFALQPYFGLTHEEVIKYIKEGNVLGCPDNTPLSVYALMRRCWNR 696

Qy        810 EPQQRLNIKEI-YKILHALGKA 830
              :| :|    || : | |:: ::
Db        697 KPSERPGFAEINHCIQHSIAES 718


RESULT 15
ROR2_HUMAN
ID   ROR2_HUMAN     STANDARD;      PRT;   943 AA.
AC   Q01974; Q9HAY7; Q9HB61;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Tyrosine-protein kinase transmembrane receptor ROR2 precursor
DE   (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2).
GN   ROR2 OR NTRKR2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93100347; PubMed=1334494;
RA   Masiakowski P., Carroll R.D.;
RT   "A novel family of cell surface receptors with tyrosine kinase-like
RT   domain.";
RL   J. Biol. Chem. 267:26181-26190(1992).
RN   [2]
RP   SEQUENCE OF 34-943 FROM N.A., AND VARIANT ILE-819.
RX   MEDLINE=20164326; PubMed=10700182;
RA   Oldridge M., Fortuna A.M., Maringa M., Propping P., Mansour S.,
RA   Pollitt C., DeChiara T.M., Kimble R.B., Valenzuela D.M.,
RA   Yancopoulos G.D., Wilkie A.O.M.;
RT   "Dominant mutations in ROR2, encoding an orphan receptor tyrosine
RT   kinase, cause brachydactyly type B.";
RL   Nat. Genet. 24:275-278(2000).
RN   [3]
RP   SEQUENCE OF 34-574 FROM N.A., AND VARIANT THR-245.
RX   MEDLINE=20442029; PubMed=10986040;
RA   Schwabe G.C., Tinschert S., Buschow C., Meinecke P., Wolff G.,
RA   Gillessen-Kaesbach G., Oldridge M., Wilkie A.O.M., Koemec R.,
RA   Mundlos S.;
RT   "Distinct mutations in the receptor tyrosine kinase gene ROR2 cause
RT   brachydactyly type B.";
RL   Am. J. Hum. Genet. 67:822-831(2000).
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RN   [4]
RP   VARIANTS RRS CYS-184; TRP-189; TRP-366 AND LYS-620.
RX   MEDLINE=20392394; PubMed=10932186;
RA   Afzal A.R., Rajab A., Fenske C.D., Oldridge M., Elanko N.,
RA   Ternes-Pereira E., Tueysuez B., Murday V.A., Patton M.A.,
RA   Wilkie A.O.M., Jeffery S.;
RT   "Recessive Robinow syndrome, allelic to dominant brachydactyly type B,
RT   is caused by mutation of ROR2.";
RL   Nat. Genet. 25:419-422(2000).
RN   [5]
RP   VARIANT RRS TYR-182.
RX   MEDLINE=20392395; PubMed=10932187;
RA   van Bokhoven H., Celli J., Kayserili H., van Beusekom E., Balci S.,
RA   Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.G.;
RT   "Mutation of the gene encoding the ROR2 tyrosine kinase causes
RT   autosomal recessive Robinow syndrome.";
RL   Nat. Genet. 25:423-426(2000).
RN   [6]
RP   ERRATUM.
RA   van Bokhoven H., Celli J., Kayserili H., van Beusekom E., Balci S.,
RA   Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.G.;
RL   Nat. Genet. 26:383-383(2000).
CC   -!- FUNCTION: Tyrosine-protein kinase receptor which may be involved
CC       in the early formation of the chondrocytes. It seems to be
CC       required for cartilage and growth plate development.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC       tyrosine phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- DEVELOPMENTAL STAGE: Expressed at high levels during early
CC       embryonic development. The expression levels drop strongly around
CC       day 16 and there are only very low levels in adult tissues.
CC   -!- DISEASE: Defects in ROR2 are a cause of brachydactyly type B1
CC       (BDB1) [MIM:113000]. BDB1 is an autosomal dominant skeletal
CC       disorder characterized by hypoplasia/aplasia of distal phalanges
CC       and nails. In BDB1 the middle phalanges are short but in addition
CC       the terminal phalanges are rudimentary or absent. Both fingers and
CC       toes are affected. The thumbs and big toes are usually deformed.
CC   -!- DISEASE: Defects in ROR2 are a cause of recessive Robinow syndrome
CC       (RRS) [MIM:268310]. RRS is an autosomal disorder characterized by
CC       skeletal dysplasia with generalized limb bone shortening,
CC       segmental defects of the spine, brachydactyly and a dysmorphic
CC       facial appearance.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
CC       subfamily.
CC   -!- SIMILARITY: Contains 1 frizzled (FZ) domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- SIMILARITY: Contains 1 kringle domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M97639; AAA60276.1; -.
DR   EMBL; AF294796; AAG01184.2; -.
DR   EMBL; AF254747; AAG01184.2; JOINED.
DR   EMBL; AF254748; AAG01184.2; JOINED.
DR   EMBL; AF254749; AAG01184.2; JOINED.
DR   EMBL; AF254750; AAG01184.2; JOINED.
DR   EMBL; AF254751; AAG01184.2; JOINED.
DR   EMBL; AF254752; AAG01184.2; JOINED.
DR   EMBL; AF254753; AAG01184.2; JOINED.
DR   EMBL; AF279762; AAG33132.1; -.
DR   EMBL; AF279755; AAG33132.1; JOINED.
DR   EMBL; AF279756; AAG33132.1; JOINED.
DR   EMBL; AF279757; AAG33132.1; JOINED.
DR   EMBL; AF279758; AAG33132.1; JOINED.
DR   EMBL; AF279759; AAG33132.1; JOINED.
DR   EMBL; AF279760; AAG33132.1; JOINED.
DR   EMBL; AF279761; AAG33132.1; JOINED.
DR   PIR; B45082; B45082.
DR   HSSP; P00747; 1KRN.
DR   Genew; HGNC:10257; ROR2.
DR   MIM; 602337; -.
DR   MIM; 113000; -.
DR   MIM; 268310; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; TAS.
DR   GO; GO:0007275; P:development; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR000024; Fz_domain.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000001; Kringle.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF01392; Fz; 1.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00051; kringle; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00018; KRINGLE.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000395; Kringle; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00130; KR; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50038; FZ; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00021; KRINGLE_1; 1.
DR   PROSITE; PS50070; KRINGLE_2; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Transferase; Tyrosine-protein kinase; ATP-binding; Receptor;
KW   Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
KW   Immunoglobulin domain; Developmental protein; Polymorphism;
KW   Disease mutation.
FT   SIGNAL       1     33       POTENTIAL.
FT   CHAIN       34    943       TYROSINE-PROTEIN KINASE TRANSMEMBRANE
FT                               RECEPTOR ROR2.
FT   DOMAIN      34    403       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   404    424       POTENTIAL.
FT   DOMAIN     425    943       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      55    145       IG-LIKE C2-TYPE.
FT   DOMAIN     169    303       FZ.
FT   DOMAIN     316    394       KRINGLE.
FT   DOMAIN     473    746       PROTEIN KINASE.
FT   DOMAIN     753    782       SER/THR-RICH.
FT   DOMAIN     784    857       PRO-RICH.
FT   DOMAIN     859    882       SER/THR-RICH.
FT   NP_BIND    479    487       ATP (BY SIMILARITY).
FT   BINDING    507    507       ATP (BY SIMILARITY).
FT   ACT_SITE   615    615       BY SIMILARITY.
FT   MOD_RES    646    646       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   DISULFID    83    135       BY SIMILARITY.
FT   CARBOHYD    70     70       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   188    188       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   318    318       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT    182    182       C -> Y (in RRS).
FT                               /FTId=VAR_010911.
FT   VARIANT    184    184       R -> C (in RRS).
FT                               /FTId=VAR_010768.
FT   VARIANT    189    189       R -> W (in RRS).
FT                               /FTId=VAR_010769.
FT   VARIANT    245    245       A -> T.
FT                               /FTId=VAR_010912.
FT   VARIANT    366    366       R -> W (in RRS).
FT                               /FTId=VAR_010770.
FT   VARIANT    620    620       N -> K (in RRS).
FT                               /FTId=VAR_010771.
FT   VARIANT    819    819       V -> I.
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FT                                /FTId=VAR_010913.
SQ   SEQUENCE   943 AA;  104726 MW;  DBAC1E4622B5ECA0 CRC64;

  Query Match           14.8%;  Score 666;  DB 1;  Length 943;
  Best Local Similarity   26.7%;  Pred. No. 1.8e-33;
  Matches  205;  Conservative   98;  Mismatches  221;  Indels  244;  Gaps   26;

Qy        218 NLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSED 277
              |:|: :|  |:: |  :|:| |:| |:      :  :  :     :   | : :: : |
Db         70 NITIVQGQTAILHCKVAGNPPPNVRWLKNDAPVVQEPRRIIIRKTEYGSRLRIQDLDTTD 129

Qy        278 NGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEH---------------CIE 322
              |:  |:| | :   |:  | |   |:     |    :                   |
Db        130 TGY-YQCVATNGMKTITATGVLFV----RLGPTHSPNHNFQDDYHEDGFCQPYRGIACAR 184

Qy        323 FVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQ-EGEI-----------------SEGCLL 364
              |:  ||                : |:|:  | :|||                  |: |
Db        185 FI--GN-----------------RTIYVDSLQMQGEIENRITAAFTMIGTSTHLSDQCSQ 225

Qy        365 FNKPT--HY----------------------------NNGNYTLIAKNPL--------- 384
              |  |:  |:                          ||:   |||
Db        226 FAIPSFCHFVFPLCDARSRAPKPRELCRDECEVLESDLCRQEYTIARSNPLILMRLQLPK 285

Qy        385 ----------------------------------------GTANQTINGH-----FLKEP 399
                                                     |||: | :||      |: |
Db        286 CEALPMPESPDAANCMRIGIPAERLGRYHQCYNGSGMDYRGTASTTKSGHQCQPWALQHP 345

Qy        400 ---------FPE-------------------STDNFILFDEVSPTPPITVTHKPEEDT- 429
                     |||                   | |  :  |:   |  :    | : :
Db        346 HSHHLSSTDFPELGGGHAYCRNPGGQMEGPWCFTQNKNVRMELCDVPSCS----PRDSSK 401

Qy        430 PGV------SIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASPLHH 483
              |:       |||: |   ||:  :|          |:|              :: |||
Db        402 MGILYILVPSIAIPL-VIACLFFLVCMC-------RNK------------QKASAS---- 437

Qy        484 INHGITTPS--SLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVLK 541
                  ||    | | |   :     :|:|          | ||    :: |    :
Db        438 ------TPQRRQLMASPSQDM----EMPLI----------NQHK-QAKLKEISLSAVRFM 476

Qy        542 RELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLA-ARKDFQREAELLTNLQHEHI 600
              ||||  ||||:    :  :| :    ||:| |||      |::|: || |   ||| ::
Db        477 EELGEDRFGKVYKGHLFGPAPGEQTQAVAIKTLKDKAEGPLREEFRHEAMLRARLQHPNV 536

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              |   ||      || |:| |  ||||::||     | : :      |  |  |     :|:
Db        537 VCLLGVVTKDQPLSMIFSYCSHGDLHEFLVMRSPHSDVGSTDDDRTVKSALEPPDFVHLV 596

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              :|||:|| ||:|  | ||:|||||| ||   | ||| | |: |:||: |||:|
Db        597 AQIAAGMEYLSSHHVVHKDLATRNVLVYDKLNVKISDLGLFREVYAADYYKLL------- 649

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
                  |:::|||||| ||:||| ||: :||:||:||:|||:|:|| ||:   || :|:
Db        650 -------GNSLLPIRWMAPEAIMYGKFSIDSDIWSYGVVLWEVFSYGLQPYCGYSNQDVV 702

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALG 828
              | |   :||  |  ||  || :|: ||   | :|   |:|:  | | |
Db        703 EMIRNRQVLPCPDDCPAWVYALMIECWNEFPSRRPRFKDIHSRLRAWG 750


Search completed: July 12, 2004, 13:37:48
Job time : 21 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:32:05 ; Search time 51 Seconds
(without alignments)
5190.584 Million cell updates/sec

Title: US-09-966-147-6
Perfect score: 4497
Sequence: 1 MDVSLCPAKCSFWRIFLLGS.....IYKILHALGKATPIYLDILG 839

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4492	99.9	839	4	O75682	O75682 homo sapien
2	2831	63.0	612	4	Q96CY4	Q96cy4 homo sapien
3	2720	60.5	612	11	Q9Z2P9	Q9z2p9 mus musculu
4	2379	52.9	502	11	Q9Z2Q0	Q9z2q0 mus musculu
5	2313	51.4	811	13	Q9YH43	Q9yh43 xenopus lae
6	2308	51.3	821	13	Q9YH44	Q9yh44 xenopus lae
7	2259	50.2	838	4	Q8WXJ7	Q8wxj7 homo sapien
8	2013	44.8	790	13	Q90699	Q90699 gallus gall
9	1678	37.3	486	13	Q9PST9	Q9pst9 xenopus lae
10	1375.5	30.6	591	4	Q15656	Q15656 homo sapien
11	1247.5	27.7	503	4	Q15655	Q15655 homo sapien
12	1216	27.0	282	13	Q91373	Q91373 xenopus. tr
13	979.5	21.8	537	4	Q8WXJ6	Q8wxj6 homo sapien
14	961.5	21.4	553	4	Q8WXJ5	Q8wxj5 homo sapien
15	884	19.7	168	6	Q9GL47	Q9gl47 cercopithec
16	823	18.3	160	6	Q9GMA2	Q9gma2 cercopithec
17	801	17.8	868	11	Q62838	Q62838 rattus norv
18	795.5	17.7	869	4	O15146	O15146 homo sapien
19	793.5	17.6	871	11	Q61987	Q61987 mus musculu
20	793.5	17.6	881	11	Q61988	Q61988 mus musculu
21	792	17.6	860	11	Q61005	Q61005 mus musculu
22	788	17.5	868	11	Q61006	Q61006 mus musculu
23	783.5	17.4	476	13	Q7ZXJ8	Q7zxj8 xenopus lae
24	778	17.3	572	5	Q7YWD8	Q7ywd8 lymnaea sta
25	773	17.2	476	11	Q91XJ9	Q91xj9 mus musculu
26	772	17.2	465	11	Q80WU0	Q80wu0 mus musculu
27	754	16.8	946	13	Q07153	Q07153 torpedo cal
28	739.5	16.4	947	13	Q8AXY6	Q8axy6 gallus gall
29	693.5	15.4	354	13	Q9DDA2	Q9dda2 xenopus lae
30	692.5	15.4	948	5	Q9Y1Y6	Q9y1y6 ephydatia f
31	692.5	15.4	1145	5	Q9BKL8	Q9bkl8 aplysia cal
32	684	15.2	553	13	Q7ZZ92	Q7zz92 brachydanio
33	683	15.2	162	11	Q9WU17	Q9wu17 mesocricetu
34	659	14.7	944	11	Q8C3W2	Q8c3w2 mus musculu
35	653.5	14.5	855	4	Q7Z730	Q7z730 homo sapien
36	652	14.5	944	11	Q8BSP6	Q8bsp6 mus musculu
37	647	14.4	937	11	Q8BNP9	Q8bnp9 mus musculu
38	647	14.4	937	11	Q8BG10	Q8bg10 mus musculu
39	644.5	14.3	168	13	Q91407	Q91407 brachydanio
40	641	14.3	840	11	Q99P57	Q99p57 cricetulus
41	640.5	14.2	940	4	Q8NFA7	Q8nfa7 homo sapien
42	639.5	14.2	804	5	Q7YT64	Q7yt64 crassostrea
43	633.5	14.1	909	6	Q7YR43	Q7yr43 pan troglod
44	631.5	14.0	930	13	Q8AV69	Q8av69 xenopus lae
45	629	14.0	1062	11	Q8BKG3	Q8bkg3 mus musculu

ALIGNMENTS

RESULT 1
O75682
ID O75682 PRELIMINARY; PRT; 839 AA.
AC O75682;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TRKC protein (EC 2.7.1.112) (Tyrosine-protein kinase
DE receptor).
GN TRKC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98449483; PubMed=9778053;
RA Ichaso N., Rodriguez R., Martin-Zanca D., Gonzalez-Sarmiento R.;
RT "Genomic characterization of the human trkC gene.";
RL Oncogene 17:1871-1875(1998).
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC RECEPTOR SUBFAMILY.
DR EMBL; AJ224521; CAA12029.1; -.
DR EMBL; AJ224522; CAA12029.1; JOINED.
DR EMBL; AJ224523; CAA12029.1; JOINED.
DR EMBL; AJ224524; CAA12029.1; JOINED.
DR EMBL; AJ224525; CAA12029.1; JOINED.
DR EMBL; AJ224526; CAA12029.1; JOINED.
DR EMBL; AJ224527; CAA12029.1; JOINED.
DR EMBL; AJ224528; CAA12029.1; JOINED.
DR EMBL; AJ224529; CAA12029.1; JOINED.
DR EMBL; AJ224530; CAA12029.1; JOINED.
DR EMBL; AJ224531; CAA12029.1; JOINED.
DR EMBL; AJ224532; CAA12029.1; JOINED.
DR EMBL; AJ224533; CAA12029.1; JOINED.
DR EMBL; AJ224534; CAA12029.1; JOINED.

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DR   EMBL; AJ224535; CAA12029.1; JOINED.
DR   HSSP; P06213; 1IRK.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
SQ   SEQUENCE   839 AA;  94428 MW;  7FE88468300083C08 CRC64;

  Query Match             99.9%;  Score 4492;  DB 4;  Length 839;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  838;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVL 540

Qy        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 KRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHI 600

Qy        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 VKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIA 660

Qy        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 SQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDF 720

Qy        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVI 780

Qy        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839


RESULT 2
Q96CY4
ID   Q96CY4      PRELIMINARY;      PRT;   612 AA.
AC   Q96CY4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Neurotrophic tyrosine kinase, receptor, type
DE   3).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) System Donor
RT   vector.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013693; AAH13693.1; -.
DR   EMBL; BT007291; AAP35955.1; -.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hypothetical protein; Kinase; Receptor.
SQ   SEQUENCE   612 AA;  68452 MW;  F2E84DC71B8E4DB3 CRC64;

  Query Match             63.0%;  Score 2831;  DB 4;  Length 612;
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  Best Local Similarity   99.6%;  Pred. No. 8.5e-225;
  Matches  528;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYV 530
              |||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTWV 530


RESULT 3
Q9Z2P9
ID   Q9Z2P9      PRELIMINARY;      PRT;   612 AA.
AC   Q9Z2P9;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Neurotrophin-3 receptor non-catalytic isoform 2.
GN   NTRK3 OR TRKC.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57 Black/6; TISSUE=Brain;
RX   MEDLINE=99017700; PubMed=9802700;
RA   Menn B., Timsit S., Calothy G., Lamballe F.;
RT   "Differential expression of TrkC catalytic and noncatalytic isoforms
RT   suggests that they act independently or in association.";
RL   J. Comp. Neurol. 401:47-64(1998).
DR   EMBL; AF035400; AAC72290.1; -.
DR   MGD; MGI:97385; Ntrk3.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Receptor.
SQ   SEQUENCE   612 AA;  68387 MW;  376F0F449792CE46 CRC64;

  Query Match           60.5%;  Score 2720;  DB 11;  Length 612;
  Best Local Similarity   95.3%;  Pred. No. 1.3e-215;
  Matches  505;  Conservative   15;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRGLHTLNAVDMELYTGLQKLTIKNSGLRNIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              :|:||:||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RLDSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              |||||||||| |||:|||||||||||||| |||||:||||||||::|||||:||
Db        301 VYYPPRVVSLVEPEVRLEHCIEFVVRGNPTPTLHWLYNGQPLRESKIIHMDYYQEGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              |||||||||||||||||||| |||||||||||||||| |     : |||||||
Db        361 GCLLFNKPTHYNNGNYTLIAKNALGTANQTINGHFLKEPFPESTDFFDFESDASPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASP 480
              ||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSASP 480

Qy        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYV 530
              |||||||||||||||||||||||||||||||||||||||||||||||||:|
Db        481 LHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTWV 530


RESULT 4
Q9Z2Q0
ID   Q9Z2Q0      PRELIMINARY;      PRT;   502 AA.
AC   Q9Z2Q0;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Neurotrophin-3 receptor non-catalytic isoform 1.
GN   NTRK3 OR TRKC.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57 Black/6; TISSUE=Brain;
RX   MEDLINE=99017700; PubMed=9802700;
RA   Menn B., Timsit S., Calothy G., Lamballe F.;
RT   "Differential expression of TrkC catalytic and noncatalytic isoforms
RT   suggests that they act independently or in association.";
RL   J. Comp. Neurol. 401:47-64(1998).
DR   EMBL; AF035399; AAC72289.1; -.
DR   MGD; MGI:97385; Ntrk3.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR001064; Crystallin.
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DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Receptor.
SQ   SEQUENCE   502 AA;  56366 MW;  51BA2A88D7AF549D CRC64;

  Query Match             52.9%;  Score 2379;  DB 11;  Length 502;
  Best Local Similarity   93.3%;  Pred. No. 1.4e-187;
  Matches  443;  Conservative   15;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDVSLCPAKCSFWRIFLLGSVWLDYVGSVLACPANCVCSKTEINCRRPDDGNLFPLLEGQ 60

Qy         61 DSGNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQP 120
              |||||||||:||||||||||||||||| ||||||||||||||||||||||||:|||
Db         61 DSGNSNGNASINITDISRNITSIHIENWRGLHTLNAVDMELYTGLQKLTIKNSGLRNIQP 120

Qy        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEA 180
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        121 RAFAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELRLEQNFFNCSCDIRWMQLWQEQGEA 180

Qy        181 KLNSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240
              :|:||:||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RLDSQSLYCISADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPD 240

Qy        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VDWIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALT 300

Qy        301 VYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISE 360
              |||||||||| |||:|||||||||||||| |||||:||||||||||::|||||:||
Db        301 VYYPPRVVSLVEPEVRLEHCIEFVVRGNPTPTLHWLYNGQPLRESKIIHMDYYQEGEVSE 360

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPIT 420
              ||||| |||||||||||||||| ||||||||||||||||||| |    : |||||||
Db        361 GCLLFKKPTHYNNGNYTLIAKNALGTANQTINGHFLKEPFPESTDFFDFESDASPTPPIT 420

Qy        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEE 475
              |||||||||||||||||||||||||||:|||||||||||||| |     :|
Db        421 VTHKPEEDTFGVSIAVGLAAFACVLLVVLFIMINKYGRRSKFGMKGKVLFFQSQE 475


RESULT 5
Q9YH43
ID   Q9YH43      PRELIMINARY;      PRT;   811 AA.
AC   Q9YH43;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Neurotrophin receptor B xTrkB-alpha (EC 2.7.1.112) (Tyrosine-protein
DE   kinase receptor).
GN   XTRKB.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97101727; PubMed=8946245;
RA   Islam N., Gagnon F., Moss T.;
RT   "Catalytic and non-catalytic forms of the neurotrophin receptor xTrkB
RT   mRNA are expressed in a pseudo-segmental manner within the early
RT   Xenopus central nervous system.";
RL   Int. J. Dev. Biol. 40:973-983(1996).
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC       TYROSINE PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC       RECEPTOR SUBFAMILY.
DR   EMBL; U39671; AAD00002.1; -.
DR   HSSP; P06213; 1IRK.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; Recepttyrkinsii.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00560; LRR; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
SQ   SEQUENCE   811 AA;  91249 MW;  CE7CD1CF132C1CF5 CRC64;

  Query Match             51.4%;  Score 2313;  DB 13;  Length 811;
  Best Local Similarity   55.8%;  Pred. No. 8.1e-182;
  Matches  464;  Conservative  114;  Mismatches  206;  Indels   48;  Gaps   11;

Qy         19 GSVW--LDYVGSVLACPANCVCSKTEINCRRPDDG-NLFPLLEGQDSGNSNGNANINITD 75
              |::|  |      ||||  | |: | | |   | |  ||:||                :
Db         17 GALWILLALFWRGLACPQYCSCNSTRIWCTLMDKGIAAFPVLED-------------SS 62

Qy         76 ISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLS 135
              :: ||| |:| | ||| ::|  |:::|||| :|: :|||: :  :|| ||  | ||| |
Db         63 LAENITDIYIANQRSLASINDDDVKIYTGLRNLTVVDSGLQIVSRQAFRKNLKLTYINFS 122

Qy        136 SNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGS 195
               |:||:|: ::|: |:| :| |  | | |||: |:::  |      : :||::| | :
Db        123 RNKLTSLTKKIFRHLTLSQLLLGGNPFQCSCDLMWVKVLLETNSLNMENQNIHCFNDNKK 182

Qy        196 QLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQ 255
              ::||| |:|  | ||  :|| ||:|| ||:   : |: :| | |:| | ::  | |:  :
Db        183 KIPLFNMHIPNCGLPIANVSTVNITVLEGNETTLYCDANGLPDPNVSWDIS--QIISKKR 240

Qy        256 TNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPEL 315
               :       : ||| |||| ||   : |:||| ||  : || | |::|| :  :: | |
Db        241 MEM---AKRPVLLTLKNVTSLDNKRIIVCVAENSVGEDHISVELNVHFPPVITFIDLPTL 297

Qy        316 RLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEIS---EGCLLFNKPTHYN 372
                 || | ||||| ||| | | |  | |:  | : ::    :    |||  : ||| |
Db        298 DHHWCIPFSVRGNPKPTLQWFHEGNILSETDFIWSKIHETSNYTSEHHGCLQLDSPTHLN 357

Qy        373 NGNYTLIAKNPLGTANQTINGHFLKEPFP--ESTDNFILFDEVSPTPPIT---VTHKPEE 427
              || ||| |:|  |   ::|:  |:| |     |:| | |           :|   |::  |
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Db        358 NGFYTLRAENIYGRDERSISALFMKGPDDDYETTSNDIGGTSTDIGTGVTSTDVSNGGNE 417

Qy        428 DTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHG 487

Db        418 DSITVYVVVGIAAALVCTGLVIMLIIL-KFGRHSKFGLKGPSSVISNDDDSASPLHHISNG 476

Qy        488 ITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEG 547

Db        477 SNTPSSSEGGPDTVIIGMTKIPVIENPQYFGITNSHLKSDTFVQHIKRHNIVLKRELGEG 536

Qy        548 AFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVC 607

Db        537 AFGKVFLAECYNLYPEQDKILVAVKTLKDASDNARKDFHREAELLTNLQHEHIVKFYGVC 596

Qy        608 GDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGM 667

Db        597 VEGDPLIMVFEYMKHGDLNKFLRAHGPDAVLMAEG---NRPAELTQSQMLHIAQQIAAGM 653

Qy        668 VYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVG 727

Db        654 VYLASQHFVHRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYYR--------------VG 699

Qy        728 GHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGR 787

Db        700 GHTMLPIRWMPPESIMYRKFTTESDVWSLGVVLWEIFTYGKQPWYQLSNNEVIECITQGR 759

Qy        788 VLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839

Db        760 VLQRPRTCPKEVYDLMLGCWQREPHMRLNIKEIHSLLQNLSKASPVYLDILG 811


RESULT 6
Q9YH44
ID   Q9YH44      PRELIMINARY;      PRT;   821 AA.
AC   Q9YH44;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Neurotrophin receptor B xTrkB-alpha (EC 2.7.1.112) (Tyrosine-protein
DE   kinase receptor).
GN   XTRKB.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97101727; PubMed=8946245;
RA   Islam N., Gagnon F., Moss T.;
RT   "Catalytic and non-catalytic forms of the neurotrophin receptor xTrkB
RT   mRNA are expressed in a pseudo-segmental manner within the early
RT   Xenopus central nervous system.";
RL   Int. J. Dev. Biol. 40:973-983(1996).
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC       TYROSINE PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC       RECEPTOR SUBFAMILY.
DR   EMBL; U39670; AAD00001.1; -.
DR   HSSP; P06213; 1IRK.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00560; LRR; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
SQ   SEQUENCE   821 AA;  92311 MW;  0AF81BE74FD8FED3 CRC64;

  Query Match           51.3%;  Score 2308;  DB 13;  Length 821;
  Best Local Similarity  55.1%;  Pred. No. 2.1e-181;
  Matches  464;  Conservative  114;  Mismatches  206;  Indels   58;  Gaps   11;

Qy         19 GSVW--LDYVGSVLACPANCVCSKTEINCRRPDDG-NLFPLLEGQDSGNSNGNANINITD 75

Db         17 GALWILLALFWRGLACPQYCSCNSTRIWCTLMDKGIAAFPVLED--------------SS 62

Qy         76 ISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLS 135

Db         63 LAENITDIYIANQRSLASINDDDVKIYTGLRNLTVVDSGLQIVSRQAFRKNLKLTYINFS 122

Qy        136 SNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGS 195

Db        123 RNKLTSLTKKIFRHLTLSQLLLGGNPFQCSCDLMWVKVLLETNSLNMENQNIHCFNDNKK 182

Qy        196 QLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQ 255

Db        183 KIPLFNMHIPNCGLPIANVSTVNITVLEGNETTLYCDANGLPDPNVSWDIS--QIISKKR 240

Qy        256 TNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPEL 315

Db        241 MEM---AKRPVLLTLKNVTSLDNKRIIVCVAENSVGEDHISVELNVHFPPVITFIDLPTL 297

Qy        316 RLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEIS---EGCLLFNKPTHYN 372

Db        298 DHHWCIPFSVRGNPKPTLQWFHEGNILSETDFIWSKIHETSNYTSEHHGCLQLDSPTHLN 357

Qy        373 NGNYTLIAKNPLGTANQTINGHFLKEPFP-----------ESTDNFILFDEVSPTPPIT 420

Db        358 NGFYTLRAENIYGRDERSISALFMKGPDDGNPITDPGFYDYETTSNDIGGTSTDIGTGVT 417

Qy        421 ---VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDS 477

Db        418 STDVSNGGNEDSITVYVVVGIAALVCTGLVIMLIIL-KFGRHSKFGLKGPSSVISNDDDS 476

Qy        478 ASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRD 537

Db        477 ASPLHHISNGSNTPSSSEGGPDTVIIGMTKIPVIENPQYFGITNSHLKSDTFVQHIKRHN 536

Qy        538 IVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQH 597

Db        537 IVLKRELGEGAFGKVFLAECYNLYPEQDKILVAVKTLKDASDNARKDFHREAELLTNLQH 596

Qy        598 EHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQML 657

Db        597 EHIVKFYGVCVEGDPLIMVFEYMKHGDLNKFLRAHGPDAVLMAEG---NRPAELTQSQML 653

Qy        658 HIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSG 717

Db        654 HIAQQIAAGMVYLASQHFVHRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYYR------ 707

Qy        718 NDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNT 777
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                    |||||||||||||||||||||||||||||||| ||:||||||||||||:||||
Db        708 --------VGGHTMLPIRWMPPESIMYRKFTTESDVWSLGVVLWEIFTYGKQPWYQLSNN 759

Qy        778 EVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDI 837
              |||||||||||:||| |||||||:||||||||  |||||||: :|  | ||:|:|||| |
Db        760 EVIECITQGRVLQRPRTCPKEVYDLMLGCWQREPHMRLNIKEIHSLLQNLSKASPVYLDI 819

Qy        838 LG 839
              ||
Db        820 LG 821


RESULT 7
Q8WXJ7
ID   Q8WXJ7      PRELIMINARY;      PRT;   838 AA.
AC   Q8WXJ7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Neurotrophin receptor tyrosine kinase type 2 (EC 2.7.1.112) (Tyrosine-
DE   protein kinase receptor).
GN   NTRK2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21656983; PubMed=11798182;
RA   Stoilov P., Castren E., Stamm S.;
RT   "Analysis of the Human TrkB Gene Genomic Organization Reveals Novel
RT   TrkB Isoforms, Unusual Gene Length, and Splicing Mechanism.";
RL   Biochem. Biophys. Res. Commun. 290:1054-1065(2002).
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC       TYROSINE PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC       RECEPTOR SUBFAMILY.
DR   EMBL; AF410899; AAL67965.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   ATP-binding; Glycoprotein; Immunoglobulin domain; Kinase;
KW   Phosphorylation; Receptor; Transferase; Transmembrane;
KW   Tyrosine-protein kinase.
SQ   SEQUENCE   838 AA;  93825 MW;  130C95A9D8895432 CRC64;

  Query Match           50.2%;  Score 2259;  DB 4;  Length 838;
  Best Local Similarity   52.7%;  Pred. No. 2.5e-177;
  Matches  467;  Conservative  110;  Mismatches  199;  Indels  110;  Gaps   19;

Qy          7 PAKCSFWRIFLLGSVWLDYVG---SVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDS 62
              ||    |     |  ||  ||   :  ||| :| || : | |  |  | : || ||
Db         10 PAMARLW-----GFCWL-VVGFWRAAFACPTSCKCSASRIWCSDPSPGIVAFPRLEP--- 60

Qy         63 GNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRA 122
                  |  |  ||| | | | : |   :|  |:| | ||: ||| :|||: :  :|
Db         61 ---------NSVD-PENITEIFIANQKRLEIINEDDVEAYVGLRNLTIVDSGLKFVAHKA 110

Qy        123 FAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKL 182
              | || :|::|| : |:||:|| : |: | | || |  | | ||||| |::  ||  ::
Db        111 FLKNSNLQHINFTRNKLTSLSRKHFRHLDLSELILVGNPFTCSCDIMWIKTLQE-AKSSP 169

Qy        183 NSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVD 242
              ::|:|||:|     :||  : |  | ||  ::: |||| || :  ::|: :| |:|::
Db        170 DTQDLYCLNESSKNIPLANLQIPNCGLPSANLAAPNLTVEEGKSITLSCSVAGDPVPNMY 229

Qy        243 WIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVY 302
              | |  | |      ::| :|  :  :| : |::|:|:|  ::|:|||:||    || |||:
Db        230 WDVGNLVS-----KHMNETSHTQGSLRITNISSDDSGKQISCVAENLVGEDQDSVNLTVH 284

Qy        303 YPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKII--------HVEYYQ 354
              : | :  || |      || | |:||| | | | :||  | ||| |         | ||:
Db        285 FAPTITFLESPTSDHHWCIPFTVKGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYH- 343

Qy        355 EGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEP---------FPESTD 405
                |||  : ||| |||:|||||||  |   : |: ||:  |             :|:
Db        344 ------GCLQLDNPTHMNNGDYTLIAKNEYGKDEKQISAHFMGWPGIDDGANPNYPD--- 394

Qy        406 NFILFDEV--------------SPTPPITVTHKPEEDTFGVSIAVGLAAFA--CVLLVVL 449
                :::::                :  |   || |   :   |   | :|:   | |||:|
Db        395 --VIYEDYGTAANDIGDTTNRSNEIPSTDVTDKTGREHLSVYAVVVIASVVGFC-LLVML 451

Qy        450 FVMINKYGRRSKFGMK---------------GPVAVISGEEDSASPLHHINHGITTPSS 493
              |::  |  | ||||||                || :||| ::|||||||||::|  ||||
Db        452 FLL--KLARHSKFGMKDFSWFGFGKVKSRQGVGPASVISNDDDSASPLHHISNGSNTPSS 509

Qy        494 LDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVF 553
              : ||| |:||||:|||||||||   ::  ||||:|||||| :|||||||||||||||
Db        510 SEGGPDAVIIGMTKIPVIENPQYFGITNSQLKPDTFVQHIKRHNIVLKRELGEGAFGKVF 569

Qy        554 LAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPL 613
              ||||||| | :||:||||| ||| :  ||||| |||||||||||||||||||| :||||
Db        570 LAECYNLCPEQDKILVAVKTLKDASDNARKDFHREAELLTNLQHEHIVKFYGVCVEGDPL 629

Qy        614 IMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQ 673
              |||||||||||||||||||||||::: :| |      ||  |||||| |||:||||||||
Db        630 IMVFEYMKHGDLNKFLRAHGPDAVLMAEGNP---PTELTQSQMLHIAQQIAAGMVYLASQ 686

Qy        674 HFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLP 733
              |||||||||||||| ||||||||||||||||||||                ||||||||
Db        687 HFVHRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYYR--------------VGGHTMLP 732

Qy        734 IRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPR 793
              |||||||||||||||||||| ||:||||||||||||:|||| ||||||||||:|||
Db        733 IRWMPPESIMYRKFTTESDVWSLGVVLWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPR 792

Qy        794 VCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
              ||:|||::|||||||||  | ||| |: :|  | ||:|:||||||
Db        793 TCPQEVYELMLGCWQREPHMRKNIKGIHTLLQNLAKASPVYLDILG 838


RESULT 8
Q90699
ID   Q90699      PRELIMINARY;      PRT;   790 AA.
AC   Q90699;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
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DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tropomyosin receptor kinase (EC 2.7.1.112) (Tyrosine-protein kinase
DE   receptor).
GN   CTRKA.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Schroepel A., v Schack D., Dechant G., Barde Y.A.;
RT   "Early expression of the nerve growth factor ctrkA in chicken
RT   sympathetic and sensory ganglia.";
RL   Mol. Cell. Neurosci. 6:0-0(0).
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC       TYROSINE PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC       RECEPTOR SUBFAMILY.
DR   EMBL; U43396; AAA85289.1; -.
DR   HSSP; P11362; 1FGK.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; Recepttyrkinsll.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00560; LRR; 2.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
SQ   SEQUENCE   790 AA;  88669 MW;  AD2314608F30AD71 CRC64;

  Query Match             44.8%;  Score 2013;  DB 13;  Length 790;
  Best Local Similarity   51.9%;  Pred. No. 4.7e-157;
  Matches  431;  Conservative   93;  Mismatches  222;  Indels   84;  Gaps   15;

Qy        31 ACPANCVCSKTE-INCRRP-DDGNLFPLLEGQDSGNSNGNANINITDISRNITSIHIENW 88
             ||||:| |  :  : || |    :|  || |                :   | : |||
Db        24 ACPAHCRCPASHTLRCREPLTVSSLSALLLG----------------AHRPTDVIIENQ 66

Qy        89 RSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYINLSSNRLTTLSWQLFQ 148
               | :|   |  :   |: ||| ||||: |   ||  |  | ::||| | ||:||: ||
Db        67 ALLTSLTRDDTRMLWDLRHLTISNSGLQYISDDAFQDNHRLSHVNLSFNALTSLSWKTFQ 126

Qy       149 TLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKLNSQNLYCINADGSQL-PLFRMNISQC 207
               | |:|| || | ||||| |||:||||    |:| :|:| |   :|| |  |    :  |
Db       127 YLPLQELILEGNPFNCSCGIRWLQLWQNGSRAELGNQSLLC--WEGSMLVALDSHPLHDC 184

Qy       208 DLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVDWIVTGLQSINTHQTNLNWTNVHAIN 267
             : |   : | :: :|:||:  :||:  | |    :|::  : |  :      |  |  ||

Db       185 EPPTARIEHPDVVLRQGDSVNLTCHIWGEPSATGEWVLPHVGSEPSVTKLSEWELVLEIN 244

Qy       268 LTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVYYPPRVVSLEEPELRLEHCIEFVVRG 327
                 |::|  |   ||| ||| ||::  || | | :|| ::  | |  :   || | |
Db       245 ----NISSSLNHKDLTCRAENAVGLAEDSVMLNVTFPPVILLLSEAIPQHFWCIPFSVDS 300

Qy       328 NPPPTLHWLHNGQPLRESKIIH---VEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPL 384
             || | : || ||  | |   ||   |||     :  |||  |:||| |||||||: :|||
Db       301 NPTPRILWLFNGSMLPEGPYIHTRIVEYEPNSTVLHGCLQLNRPTHVNNGNYTLVVQNPL 360

Qy       385 GTANQTINGHFLKEPFPESTDNFILFDEVSPTPPITVTHKP--------------EEDT 429
             | | ::| | |:  ||              ||  || |:  |                :| |
Db       361 GRATRSIQGRFMDNPF-----------SFSPEEPIPVSISPLGTRNSSLEGPVETADEHT 409

Qy       430 FGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGIT 489
             ||||:|| || || : | |: : :|| | |||||:    ||:: |:| |  || :| | :
Db       410 FGVSVAVALAVFASLFLSVMLIALNKCGHRSKFGINRS-AVLAQEDDLAMSLHFMNLGSS 468

Qy       490 TPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAF 549
               || ::  | :     :  |||||||     |   :  | |::||||||| |||||||
Db       469 PVSSTESKLDGL-----KSNFIENPQYF-----C---NACVHHVQRRDIVLKWELGEGAF 515

Qy       550 GKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGD 609
             |||||||| :| | ::| ||||||||: | :|| |||||||||| ||||||||||||  :
Db       516 GKVFLAECSHLLPEQEKTLVAVKALKEVTESARLDFQREAELLTVLQHEHIVKFYGVCTE 575

Qy       610 GDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVY 669
             |:|||||||||||||:|||:|||| ||  ||  |  |:| || || ||:|||||||
Db       576 GEPLIMVFEYMKHGDLNRFLRSHGPDAKILDQGQ-GQPCGQLTLSHMLQIATQIASGMVY 634

Qy       670 LASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGH 729
             ||| |||||||||||||| :|:|||||||||:|||||                 |||
Db       635 LASLHFVHRDLATRNCLVGHDLVVKIGDFGMSRDIYSTDYYR--------------VGGR 680

Qy       730 TMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVL 789
             |||||||||||:|||||||||:|||||:|||||||||||||:|||||| |||||||| |
Db       681 TMLPIRWMPPESILYRKFTTESDIWSFGVVLWEIFTYGKQPWYQLSNTEAIECITQGREL 740

Qy       790 ERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIYLDILG 839
             |||| || ||||:|  |||||||||   |::|:  | || |  ||||||||
Db       741 ERPRTCPSEVYDIMQSCWQREPQQRQRIQDIHSRLQALVKTPPIYLDILG 790


RESULT 9
Q9PST9
ID   Q9PST9      PRELIMINARY;      PRT;   486 AA.
AC   Q9PST9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Neurotrophin receptor B xTrkB-beta (EC 2.7.1.112) (Tyrosine-protein
DE   kinase receptor) (Fragment).
GN   XTRKB.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97101727; PubMed=8946245;
RA   Islam N., Gagnon F., Moss T.;
RT   "Catalytic and non-catalytic forms of the neurotrophin receptor xTrkB
RT   mRNA are expressed in a pseudo-segmental manner within the early
RT   Xenopus central nervous system.";
RL   Int. J. Dev. Biol. 40:973-983(1996).
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC       TYROSINE PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC       RECEPTOR SUBFAMILY.
DR   EMBL; U39672; AAD09444.1; -.
DR   HSSP; P06213; 1IRK.
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DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   486 AA;  54546 MW;  645B69ABE78274F0 CRC64;

  Query Match             37.3%;  Score 1678;  DB 13;  Length 486;
  Best Local Similarity   67.4%;  Pred. No. 1e-129;
  Matches  327;  Conservative   53;  Mismatches   79;  Indels   26;  Gaps    7;

Qy        361 GCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFP--ESTDNFILFDEVSPTPP 418
              |||  : ||| ||| ||| |:|  |    ::|:  |:|  |    |:| | |
Db         22 GCLQLDSPTHLNNGFYTLRAENKYGRDERSISALFMKGPDDDYETTSNDIGGTSTDIGTG 81

Qy        419 IT---VTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEE 475
              :|    |::    |::  | : ||:||  |   ||:: ::: |:|| ||||:||| :||| ::
Db         82 VTSTDVSNGGNEESITVYVVVGIAALVCTGLVIMLIIL-KFGRHSKFGLKGPSSVISNDD 140

Qy        476 DSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQG-HNCHKPDTYVQHIK 534
              |||||||||::|  |||| : |||||:||||:|||||||||   |   |  | ||:|||||
Db        141 DSASPLHHISNGSNTPSSSEGGPDTVIIGMTKIPVIENPQYF--GITNSHLKDTFVQHIK 198

Qy        535 RRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDFQREAELLTN 594
              | :|||||||||||||||||||||||    :|:||||| ||| :  |||||  |||||||||
Db        199 RHNIVLKRELGEGAFGKVFLAECYNLYLEQDKILVAVKTLKDASDNARKDFHREAELLTN 258

Qy        595 LQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPRQAKGELGLS 654
              ||||:||||||||| :|||||||||||||||||||||||||||::: :|        || |
Db        259 LQHENIVKFYGVCVEGDPLIMVFEYMKHGDLNKFLRAHGPDAVLMAEG---NLLAELTQS 315

Qy        655 QMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYYRLFN 714
              ||:||: |||:||||||||||||||||||||||||| |||||||||||||||||||||
Db        316 QMIHISQQIAAGMVYLASQHFVHRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYYR--- 372

Qy        715 PSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFTYGKQPWFQL 774
                         |||||||||||||||||||:||||||||| ||:|||||||||||||:||
Db        373 ----------VGGHTMLPIRWMPPESIMYRRFTTESDVWSLGVVLWEIFTYGKQPWYQL 421

Qy        775 SNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILHALGKATPIY 834
              || ||||||||||||:|||  ||||:|||:||||||||  |||||||: :|   | ||:|:|
Db        422 SNNEVIECITQGRVLQRPRTCPKEIYDLMLGCWQREPHMRLNIKEIHSLLQNLSKASPVY 481

Qy        835 LDILG 839
              |||||
Db        482 LDILG 486


RESULT 10
Q15656
ID   Q15656      PRELIMINARY;      PRT;   591 AA.
AC   Q15656;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   P68 TRK-T3 oncoprotein (EC 2.7.1.112) (Tyrosine-protein kinase
DE   receptor).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96025992; PubMed=7565764;
RA   Greco A., Mariani C., Miranda C., Lupas A., Pagliardini S., Pomati M.,
RA   Pierotti M.A.;
RT   "The DNA rearrangement that generates the TRK-T3 oncogene involves a
RT   novel gene on chromosome 3 whose product has a potential coiled-coil
RT   domain.";
RL   Mol. Cell. Biol. 15:6118-6127(1995).
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC       TYROSINE PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC       RECEPTOR SUBFAMILY.
DR   EMBL; X85960; CAA59936.1; -.
DR   HSSP; P11362; 1FGK.
DR   GO; GO:0005737; C:cytoplasm; NAS.
DR   InterPro; IPR000270; OPR_PB1.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00564; PB1; 1.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00666; PB1; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
SQ   SEQUENCE   591 AA;  65851 MW;  F01F76D6C5B23C06 CRC64;

  Query Match             30.6%;  Score 1375.5;  DB 4;  Length 591;
  Best Local Similarity   62.9%;  Pred. No. 1.4e-104;
  Matches  273;  Conservative   54;  Mismatches   70;  Indels   37;  Gaps    8;

Qy        411 DEVSPT-----PPITVTHKPEEDTFGVSIAVGLAAFACVLLVVLFVMINKYGRRSKFGMK 465
              |:|| |         |:     | :|  ||||:||||| |||: |   | :::|| |||:|||:
Db        190 DQVSDTNSTSGDPV---EKKDETPFGVSVAVGLAVFACLFLSTLLLVLNKCGRRNKFGIN 246

Qy        466 GPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIPVIENPQYFRQGHNCHK 525
               | ||:: |:   |  ||  :  | ::  |   :  :   |          :|||||||
Db        247 RP-AVLAPEDGLAMSLHFMTLGGSSLSPTE-GKGSGLQG----HIIENPQYF-------- 292

Qy        526 PDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLVAVKALKDPTLAARKDF 585
               |   | |||||||||| |||||||||||||| :|| |  :|||||||||||: : :||:||
Db        293 SDACVHHIKRRDIVLKWELGEGAFGKVFLAESHNLLPEQDKMLVAVKALKEASESARQDF 352

Qy        586 QREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFLRAHGPDAMILVDGQPR 645
              |||||||| |||:|||:|:||| :| ||:|||||||:|||||:|||:|||:||||| :|  |:
Db        353 QREAELLTMLQHQHIVRFFGVCTEGRPLLMVFEYMRHGDLNRFLRSHGPDAKLLAGGED- 411

Qy        646 QAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVY 705
               | |||  |:|  :|||:|:||||||  ||||||||||||||||||  |:||||||||||:|
Db        412 VAPGPLGLGQLLAVASQVAAGMVYLAGLHFVHRDLATRNCLVGQGLVVKIGDFGMSRDIY 471

Qy        706 STDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTTESDVWSFGVILWEIFT 765
              ||||||              ||| |||||||||||||:|||||||||||||||||:|||||
Db        472 STDYYR-------------VGGRTMLPIRWMPPESILYRKFTTESDVWSFGVVLWEIFT 517

Qy        766 YGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQREPQQRLNIKEIYKILH 825
              ||||||:||||||  |:||||||  ||||| ||  |||  :| |||||||||  :||:::   |
Db        518 YGKQPWYQLSNTEAIDCITQGRELERPRACPPEVYAIMRGCWQREPQQRHSIKDVHARLQ 577
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Qy        826 ALGKATPIYLDILG 839
              || :| |:|||:||
Db        578 ALAQAPPVYLDVLG 591


RESULT 11
Q15655
ID   Q15655      PRELIMINARY;      PRT;   503 AA.
AC   Q15655;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   55 kDa protein (EC 2.7.1.112) (Tyrosine-protein kinase
DE   receptor).
GN   TRK-T1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92195650; PubMed=1532241;
RA   Greco A., Pierotti M.A., Bongarzone I., Pagliardini S., Lanzi C.,
RA   Della Porta G.;
RT   "TRK-T1 is a novel oncogene formed by the Fusion of TPR and TRK genes
RT   in human papillary thyroid Carcinomas.";
RL   Oncogene 7:237-242(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92175499; PubMed=1541391;
RA   Hill K., Boone C., Goebl M., Puccia R., Sdicu A.M., Bussey H.;
RT   "Yeast KRE2 Defines a new Gene family encoding probable secretory
RT   proteins, and is Required for correct N-Glycosylation of proteins.";
RL   Genetics 130:273-283(1992).
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC       TYROSINE PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC       RECEPTOR SUBFAMILY.
DR   EMBL; X62947; CAA44719.1; -.
DR   PIR; S23741; S23741.
DR   HSSP; P11362; 1FGK.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
SQ   SEQUENCE   503 AA;  58174 MW;  17273FF47557F2FD CRC64;

  Query Match             27.7%;  Score 1247.5;  DB 4;  Length 503;
  Best Local Similarity   70.9%;  Pred. No. 4e-94;
  Matches  234;  Conservative   35;  Mismatches   38;  Indels   23;  Gaps    3;

Qy        510 VIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLV 569
              :|||||||          |  | |||||||||| ||||||||||||||:|| | :|||||
Db        197 IIENPQYF--------SDACVHHIKRRDIVLKWELGEGAFGKVFLAECHNLLPEQDKMLV 248

Qy        570 AVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFL 629
              ||||||: : :||:|||||||||| |||:|||:|:||| :| ||:||||||:|||||:||
Db        249 AVKALKEASESARQDFQREAELLTMLQHQHIVRFFGVCTEGRPLLMVFEYMRHGDLNRFL 308

Qy        630 RAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGA 689
              |:||||| :|  |:   | | ||| |:| :|||:|:|||||  ||||||||||||||||
Db        309 RSHGPDAKLLAGGED-VAPGPLGLGQLLAVASQVAAGMVYLAGLHFVHRDLATRNCLVGQ 367

Qy        690 NLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTT 749
              |:|||||||||||:|||||||               ||| |||||||||||||:||||||
Db        368 GLVVKIGDFGMSRDIYSTDYYR-------------VGGRTMLPIRWMPPESILYRKFTT 413

Qy        750 ESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQR 809
              |||||||||:||||||||||||:|||||| |:|||||| ||||| || ||| :| |||||
Db        414 ESDVWSFGVVLWEIFTYGKQPWYQLSNTEAIDCITQGRELERPRACPPEVYAIMRGCWQR 473

Qy        810 EPQQRLNIKEIYKILHALGKATPIYLDILG 839
              ||||| :||:::  | || :| |:|||:||
Db        474 EPQQRHSIKDVHARLQALAQAPPVYLDVLG 503


RESULT 12
Q91373
ID   Q91373      PRELIMINARY;      PRT;   282 AA.
AC   Q91373;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   TrkB (EC 2.7.1.112) (Tyrosine-protein kinase receptor)
DE   (Fragment).
GN   TRKB.
OS   Xenopus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae.
OX   NCBI_TaxID=8353;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94213743; PubMed=8068082;
RA   Cohen-Cory S., Fraser S.E.;
RT   "BDNF in the development of the visual system of Xenopus.";
RL   Neuron 12:747-761(1994).
CC   -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC       TYROSINE PHOSPHATE.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
CC       RECEPTOR SUBFAMILY.
DR   EMBL; S69713; AAB30791.1; -.
DR   HSSP; P08631; 1AD5.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002011; RecepttyrkinsII.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW   ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW   Transferase; Transmembrane; Tyrosine-protein kinase.
FT   NON_TER       1      1
SQ   SEQUENCE   282 AA;  32820 MW;  FCCD690DF2D101DF CRC64;

  Query Match             27.0%;  Score 1216;  DB 13;  Length 282;
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  Best Local Similarity   77.4%;  Pred. No. 6.5e-92;
  Matches  233;  Conservative   20;  Mismatches   28;  Indels   20;  Gaps    4;

Qy        511 IENPQYFRQG-HNCHKPDTYVQHIKRRDIVLKRELGEGAFGKVFLAECYNLSPTKDKMLV 569
              |||||||  |  | |  ||:|||||| :|||||||||||||||||||||||   :||:||
Db          1 IENPQYF--GITNSHLKDTFVQHIKRHNIVLKRELGEGAFGKVFLAECYNLYREQDKILV 58

Qy        570 AVKALKDPTLAARKDFQREAELLTNLQHEHIVKFYGVCGDGDPLIMVFEYMKHGDLNKFL 629
              ||| ||| :  ||||| |||||||||||:||||||| :||||||||||||||||||||||
Db         59 AVKTLKDASDNARKDFHREAELLTNLQHENIVKFYGVCVEGDPLIMVFEYMKHGDLNKFL 118

Qy        630 RAHGPDAMILVDGQPRQAKGELGLSQMLHIASQIASGMVYLASQHFVHRDLATRNCLVGA 689
              |||||||::: :|       ||  |||:||: |||:|||||||||||||| |||||||
Db        119 RAHGPDAVLMAEG---NLLIELTQSQMIHISQQIAAGMVYLASQHFVHRDLPTRNCLVGE 175

Qy        690 NLLVKIGDFGMSRDVYSTDYYRLFNPSGNDFCIWCEVGGHTMLPIRWMPPESIMYRKFTT 749
              ||||||||||||||||||||||              |||||||||||||||||||:|||
Db        176 NLLVKIGDFGMSRDVYSTDYYR--------------VGGHTMLPIRWMPPESIMYRRFTT 221

Qy        750 ESDVWSFGVILWEIFTYGKQPWFQLSNTEVIECITQGRVLERPRVCPKEVYDVMLGCWQR 809
              |||||| ||:|||||||||||:|||| ||||||||||:||| ||||:||:| |||||
Db        222 ESDVWSLGVVLWEIFTYGKQPWYQLSNNEVIECITQGRVLQRPRTCPKEIYDLMRGCWQR 281

Qy        810 E 810
              |
Db        282 E 282


RESULT 13
Q8WXJ6
ID   Q8WXJ6      PRELIMINARY;      PRT;   537 AA.
AC   Q8WXJ6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Neurotrophin receptor tyrosine kinase type 2 truncated isoform.
GN   NTRK2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21656983; PubMed=11798182;
RA   Stoilov P., Castren E., Stamm S.;
RT   "Analysis of the Human TrkB Gene Genomic Organization Reveals Novel
RT   TrkB Isoforms, Unusual Gene Length, and Splicing Mechanism.";
RL   Biochem. Biophys. Res. Commun. 290:1054-1065(2002).
DR   EMBL; AF410900; AAL67966.1; -.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00082; LRRCT; 1.
DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Kinase; Receptor.
SQ   SEQUENCE   537 AA;  59166 MW;  5A8FA252A3871CC1 CRC64;

  Query Match             21.8%;  Score 979.5;  DB 4;  Length 537;
  Best Local Similarity   39.6%;  Pred. No. 6e-72;
  Matches  222;  Conservative   90;  Mismatches  171;  Indels   77;  Gaps   16;

Qy          7 PAKCSFWRIFLLGSVWLDYVG---SVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDS 62
              ||    |     |  ||  ||   :  ||| :| || : | |  |  | : || ||

Db         10 PAMARLW-----GFCWL-VVGFWRAAFACPTSCKCSASRIWCSDPSPGIVAFPRLEP--- 60

Qy         63 GNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRA 122
                  |  |   ||| | | | :  :|  |:| | ||: ||| :|||: :  :|
Db         61 ---------NSVD-PENITEIFIANQKRLEIINEDDVEAYVGLRNLTIVDSGLKFVAHKA 110

Qy        123 FAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKL 182
              | || :|::|| : |:||:|| : |: | | || |  | | ||||| |::  ||  ::
Db        111 FLKNSNLQHINFTRNKLTSLSRKHFRHLDLSELILVGNPFTCSCDIMWIKTLQE-AKSSP 169

Qy        183 NSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVD 242
              ::|:|||:|     :||  : |  | ||  ::: ||||  ||  :  ::|: :|  |:|::
Db        170 DTQDLYCLNESSKNIPLANLQIPNCGLPSANLAAPNLTVEEGKSITLSCSVAGDPVPNMY 229

Qy        243 WIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVY 302
              | |  | |       ::| |:    :| : |::|:|:|  ::|:|||:||    || |||:
Db        230 WDVGNLVS-----KHMNETSHTQGSLRITNISSDDSGKQISCVAENLVGEDQDSVNLTVH 284

Qy        303 YPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKII--------HVEYYQ 354
              : | :  || |       || | |:||| | | | :||  | ||| |          | ||:
Db        285 FAPTITFLESPTSDHHWCIPFTVKGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYH- 343

Qy        355 EGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEP---------FPESTD 405
                 |||  : ||| |||:|||||||  |   : |: ||:  |          :|:
Db        344 ------GCLQLDNPTHMNNGDYTLIAKNEYGKDEKQISAHFMGWPGIDDGANPNYPD--- 394

Qy        406 NFILFDEV--------------SPTPPITVTHKPEEDTFGVSIAVGLAAFA--CVLLVVL 449
                :::::              :  |  || |   :     |    | :|:    | |||:|
Db        395 --VIYEDYGTAANDIGDTTNRSNEIPSTDVTDKTGREHLSVYAVVVIASVVGFC-LLVML 451

Qy        450 FVMINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAGPDTVVIGMTRIP 509
              |::  |  | |||||||| :||| ::||||||||::|  |||| : ||| |:||||:||
Db        452 FLL--KLARHSKFGMKGPASVISNDDDSASPLHHISNGSNTPSSSEGGPDAVIIGMTKIP 509

Qy        510 VIENPQYFRQGHNCHKPDTY 529
              |||||||   ::  ||||:
Db        510 VIENPQYFGITNSQLKPDTW 529


RESULT 14
Q8WXJ5
ID   Q8WXJ5      PRELIMINARY;      PRT;   553 AA.
AC   Q8WXJ5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Neurotrophin receptor tyrosine kinase type 2 truncated isoform.
GN   NTRK2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21656983; PubMed=11798182;
RA   Stoilov P., Castren E., Stamm S.;
RT   "Analysis of the Human TrkB Gene Genomic Organization Reveals Novel
RT   TrkB Isoforms, Unusual Gene Length, and Splicing Mechanism.";
RL   Biochem. Biophys. Res. Commun. 290:1054-1065(2002).
DR   EMBL; AF410901; AAL67967.1; -.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR000483; LRR_Cterm.
DR   InterPro; IPR000372; LRR_Nterm.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00560; LRR; 1.
DR   Pfam; PF01463; LRRCT; 1.
DR   Pfam; PF01462; LRRNT; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00082; LRRCT; 1.
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DR   SMART; SM00013; LRRNT; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Kinase; Receptor.
SQ   SEQUENCE   553 AA;  60994 MW;  BD98221B9EE1A6C1 CRC64;

  Query Match             21.4%;  Score 961.5;  DB 4;  Length 553;
  Best Local Similarity   38.5%;  Pred. No. 1.9e-70;
  Matches  222;  Conservative   90;  Mismatches  171;  Indels   93;  Gaps   17;

Qy          7 PAKCSFWRIFLLGSVWLDYVG---SVLACPANCVCSKTEINCRRPDDGNL-FPLLEGQDS 62
              ||     |     |  ||  ||   :  ||| :| || : | |  |  | : || ||
Db         10 PAMARLW-----GFCWL-VVGFWRAAFACPTSCKCSASRIWCSDPSPGIVAFPRLEP--- 60

Qy         63 GNSNGNANINITDISRNITSIHIENWRSLHTLNAVDMELYTGLQKLTIKNSGLRSIQPRA 122
                  |  |   ||| | | | : |  :|  |:| | ||: ||| :|||: :  :|
Db         61 ---------NSVD-PENITEIFIANQKRLEIINEDDVEAYVGLRNLTIVDSGLKFVAHKA 110

Qy        123 FAKNPHLRYINLSSNRLTTLSWQLFQTLSLRELQLEQNFFNCSCDIRWMQLWQEQGEAKL 182
              | || :|::|| : |:||:|| : |: | | || |  | | ||||| |::  ||  ::
Db        111 FLKNSNLQHINFTRNKLTSLSRKHFRHLDLSELILVGNPFTCSCDIMWIKTLQE-AKSSP 169

Qy        183 NSQNLYCINADGSQLPLFRMNISQCDLPEISVSHVNLTVREGDNAVITCNGSGSPLPDVD 242
              ::|:|||:|     :||  : |  | ||  :::  |||| || :  ::|: :| |:|::
Db        170 DTQDLYCLNESSKNIPLANLQIPNCGLPSANLAAPNLTVEEGKSITLSCSVAGDPVPNMY 229

Qy        243 WIVTGLQSINTHQTNLNWTNVHAINLTLVNVTSEDNGFTLTCIAENVVGMSNASVALTVY 302
              | |  | |       ::| |:    :| : |::|:|:|  ::|:|||:||    || |||:
Db        230 WDVGNLVS-----KHMNETSHTQGSLRITNISSDDSGKQISCVAENLVGEDQDSVNLTVH 284

Qy        303 YPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKII--------HVEYYQ 354
              : | :  || |       || | |:||| | | | :||  | ||| |         | ||:
Db        285 FAPTITFLESPTSDHHWCIPFTVKGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYH- 343

Qy        355 EGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEP---------FPESTD 405
                  |||  : ||| |||:|||||||  |   : |: ||:  |             :|:
Db        344 ------GCLQLDNPTHMNNGDYTLIAKNEYGKDEKQISAHFMGWPGIDDGANPNYPD--- 394

Qy        406 NFILFDEV--------------SPTPPITVTHKPEEDTFGVSIAVGLAAFA--CVLLVVL 449
                :::::              :  |   || |   :   |   | :|:    | |||:|
Db        395 --VIYEDYGTAANDIGDTTNRSNEIPSTDVTDKTGREHLSVYAVVVIASVVGFC-LLVML 451

Qy        450 FVMINKYGRRSKFGMK---------------GPVAVISGEEDSASPLHHINHGITTPSS 493
              |::  |  | ||||||                 || :||| ::|||||||::|  ||||
Db        452 FLL--KLARHSKFGMKDFSWFGFGKVKSRQGVGPASVISNDDDSASPLHHISNGSNTPSS 509

Qy        494 LDAGPDTVVIGMTRIPVIENPQYFRQGHNCHKPDTY 529
              : ||| |:||||:|||||||||   ::  ||||:
Db        510 SEGGPDAVIIGMTKIPVIENPQYFGITNSQLKPDTW 545


RESULT 15
Q9GL47
ID   Q9GL47      PRELIMINARY;      PRT;   168 AA.
AC   Q9GL47;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Neurotrophic tyrosine kinase receptor, type 3 (Fragment).
GN   NTRK3.
OS   Cercopithecus aethiops sabaeus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=37765;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97156137; PubMed=9000456;
RA   Tam S.-Y., Elsworth J.D., Sladek J.R. Jr., Redmond D.E. Jr.,
RA   Roth R.H.;
RT   "Identification of novel variants of trkC mRNA transcripts in brain of
RT   African green monkeys.";
RL   Exp. Neurol. 143:172-176(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Tam S.-Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY005481; AAG09616.1; -.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
KW   Kinase; Receptor.
FT   NON_TER       1      1
FT   NON_TER     168    168
SQ   SEQUENCE   168 AA;  18465 MW;  65B235CBCC026FBC CRC64;

  Query Match             19.7%;  Score 884;  DB 6;  Length 168;
  Best Local Similarity   99.4%;  Pred. No. 7.7e-65;
  Matches  167;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        378 LIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVG 437
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LIAKNPLGTANQTINGHFLKEPFPESTDNFILFDEVSPTPPITVTHKPEEDTFGVSIAVG 60

Qy        438 LAAFACVLLVVLFVMINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAG 497
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db         61 LAAFACVLLVVLFIMINKYGRRSKFGMKGPVAVISGEEDSASPLHHINHGITTPSSLDAG 120

Qy        498 PDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELG 545
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PDTVVIGMTRIPVIENPQYFRQGHNCHKPDTYVQHIKRRDIVLKRELG 168


Search completed: July 12, 2004, 13:38:51
Job time : 54 secs
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